

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 09:58:01 ; Search time 1445 Seconds  
(without alignments)  
670.660 Million cell updates/sec

Title: US-10-773-678-342

Perfect score: 20  
Sequence: 1 gactcttcgaggaagcggt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 790860

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

GenEmbl:\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % |        | DB ID | Description           |
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|            |       | Match   | Length |       |                       |
| 1          | 14    | 70.0    | 20     | 6     | AR120998 Sequence     |
| 2          | 14    | 70.0    | 20     | 6     | BD272619 Antisense    |
| 3          | 14    | 70.0    | 20     | 6     | AR531367 Sequence     |
| 4          | 13    | 65.0    | 19     | 4     | DOG45501              |
| 5          | 12.8  | 64.0    | 20     | 6     | BD228539 IL-17 hom    |
| 6          | 12.8  | 64.0    | 20     | 6     | AR359764 Sequence     |
| 7          | 12.6  | 63.0    | 20     | 6     | CQ798932 Sequence     |
| 8          | 12.4  | 62.0    | 17     | 6     | A89364 Sequence 15    |
| 9          | 12.4  | 62.0    | 17     | 6     | AX672730 Sequence     |
| 10         | 12.4  | 62.0    | 17     | 6     | AX762313 Sequence     |
| 11         | 12.4  | 62.0    | 17     | 6     | BD066877 An antisense |
| 12         | 12.4  | 62.0    | 18     | 6     | AX117443 Sequence     |
| 13         | 12.4  | 62.0    | 20     | 6     | AR098941 Sequence     |
| 14         | 12.4  | 62.0    | 20     | 6     | AR164768 Sequence     |
| 15         | 12.4  | 62.0    | 20     | 6     | BD222879              |
| 16         | 12.4  | 62.0    | 20     | 6     | I79781 Sequence 77    |
| 17         | 12.4  | 62.0    | 20     | 6     | AR218732 Sequence     |
| 18         | 12.4  | 62.0    | 20     | 6     | AR223147 Sequence     |
| 19         | 12.4  | 62.0    | 20     | 6     | AR229909 Sequence     |

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| c | 25 | 12.2 | 61.0 | 19 | 6  | AX130162 | Sequence     |
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| c | 38 | 11.8 | 59.0 | 20 | 6  | AR162450 | Sequence     |
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| c | 41 | 11.6 | 58.0 | 20 | 6  | BD141875 | Polypepti    |
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| c | 68 | 11.4 | 57.0 | 17 | 6  | AR456441 | Sequence     |
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| c | 78 | 11.4 | 57.0 | 17 | 6  | AX615316 | Sequence     |
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| c | 83 | 11.4 | 57.0 | 20 | 6  | AR130109 | Sequence     |
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 94 11.2 56.0 17 6 AR464438 Sequence  
 95 11.2 56.0 17 6 AX728547 Sequence  
 96 11.2 56.0 17 6 AX760524 Sequence  
 97 11.2 56.0 18 6 BD244848 Polynucle  
 c 98 11.2 56.0 18 6 BD244849 Polynucle  
 99 11.2 56.0 18 6 AX023724 Sequence  
 c 100 11.2 56.0 18 6 AX023725 Sequence

## ALIGNMENTS

RESULT 1  
 ARI20998 ARI20998 20 bp DNA linear PAT 16-MAY-2001  
 LOCUS Sequence 19 from patent US 6159694.  
 DEFINITION ARI20998  
 ACCESSION ARI20998  
 VERSION ARI20998.1 GI:14104574  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE Unclassified.  
 1 (bases 1 to 20)  
 AUTHORS Karras,J.G.  
 TITLE Antisense modulation of stat3 expression  
 JOURNAL Patent: US 6159694-A 19 12-DEC-2000;  
 FEATURES Location/Qualifiers  
 source 1..20  
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Query Match 70.0%; Score 14; DB 6; Length 20;  
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 QY 1 GACTCTTGCAGGAA 14  
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 Db 7 GACTCTTGCAGGAA 20

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 BD272619 BD272619 20 bp DNA linear PAT 17-JUL-2003  
 LOCUS Antisense oligonucleotide modulation of STAT3 expression.  
 DEFINITION BD272619  
 ACCESSION BD272619  
 VERSION BD272619.1 GI:33082387  
 KEYWORDS JP 2002541784-A/19.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Karras,J.G.  
 TITLE Antisense oligonucleotide modulation of STAT3 expression  
 JOURNAL Patent: JP 2002541784-A 19 10-DEC-2002;  
 COMMENT ISIS PHARMACEUTICALS INC  
 OS Artificial Sequence  
 PN JP 2002541784-A/19  
 PD 10-DEC-2002  
 PF 06-APR-2000 JP 2000611544  
 PR 08-APR-1999 US 09/288461  
 PI JAMES G KARRAS  
 PC C12N15/09,A61K31/711,A61K48/00,A61P29/00,A61P35/00,  
 PC A61P37/02,  
 PC A61P43/00,C12N5/06,C12Q1/02,C12N15/00,C12N5/00 CC Antisense  
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 AR531367 AR531367 20 bp DNA linear PAT 08-OCT-2004  
 LOCUS Sequence 19 from patent US 6727064.  
 DEFINITION AR531367  
 ACCESSION AR531367  
 VERSION AR531367.1 GI:53919806  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE Unclassified.  
 1 (bases 1 to 20)  
 AUTHORS Karras,J.G.  
 TITLE Antisense oligonucleotide modulation of STAT3 expression  
 JOURNAL Patent: US 6727064-A 19 27-APR-2004;  
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 DEFINITION DOGP45501  
 ACCESSION L24340  
 VERSION L24340.1 GI:402053  
 KEYWORDS PCR identification; PCR primer; STS.  
 SEGMENT 1 of 2  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.  
 TITLE One hundred and one new simple sequence repeat-based markers for  
 the canine genome  
 JOURNAL Mamm. Genome 6 (3), 192-195 (1995)  
 MEDLINE 95268214  
 PUBMED 7749226  
 COMMENT Original source text: Canis familiaris (library: E. Ostrander, in  
 pBUEScript+) adult spleen DNA.  
 Submitted by:  
 Fred Hutchinson Cancer Research Center  
 Transplantation Biology Dept  
 1124 Columbia; Mailstop M318  
 Seattle, WA 98104, USA  
 e-mail: EOstrander@bl.gov  
 PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)  
 PCR Profile: Denaturation: 94 degrees C for 1.00 minute  
 Annealing: 55 or 59 degrees C for 0.45 minutes  
 Polymerization: 74 degrees C for 1.00 minutes

## RESULT 6

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AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 933904-A 1512 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Db 4 ACTCTTGACGAGTAG 17
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AX672730 17 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 1175 from Patent WO03004526.
ACCESSION AX672730
VERSION AX672730.1 GI:29331078
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman,A., Amson,R. and Tuijinder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversal, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1175 16-JAN-2003;
Molecular Engines Laboratories (FR)
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RESULT 10
AX762313 17 bp DNA linear PAT 25-JUN-2003
LOCUS
DEFINITION Sequence 5634 from Patent WO03040369.
ACCESSION AX762313
VERSION AX762313.1 GI:32256929
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Telerman,A., Amson,R. and Tuijinder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5634 15-MAY-2003;
Molecular Engines Laboratories (FR)
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1. .17
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Db 3 TCTTGCAGGAAGAG 16
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RESULT 11
BD066877 17 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066877
VERSION BD066877.1 GI:22612480
KEYWORDS JP 2001511000-A/1512.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 17)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1512 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1512
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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Best Local Similarity 92.9%; Pred. No. 6e+05;
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Db 4 ACTCTTGACGAGTAG 17
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RESULT 12
AX117443 18 bp DNA linear PAT 11-MAY-2001
LOCUS
DEFINITION Sequence 2566 from Patent WO0129262.
ACCESSION AX117443
VERSION AX117443.1 GI:14034394
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Picoult-Newburg,L. and Pohl,M.
AUTHORS Genotyping reagents, kits and methods of use thereof
TITLE Patent: WO 0129262-A 2566 26-APR-2001;
JOURNAL Orchid Biosciences, Inc. (US)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match          62.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 15 CTCCTGCAGGTAGC 2

RESULT 17
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DEFINITION AR218732
ACCESSION AR218732
VERSION AR218732.1 GI:233319627
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
          Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQT1--a long qt syndrome gene
JOURNAL Patent: US 6420124-A 79 16-JUN-2002;
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Qy 7 TGCAGGAGCGGCT 20
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Db 18 TGCAGGAGCGGAT 5

RESULT 18
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DEFINITION AR223147
ACCESSION AR223147
VERSION AR223147.1 GI:23331000
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human mink which cause
          arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6432644-A 79 13-AUG-2002;
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 18 TGCAGGAGCGGAT 5

RESULT 19
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DEFINITION AR229909
ACCESSION AR229909
VERSION AR229909.1 GI:27269787
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
          Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6451534-A 79 17-SEP-2002;
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Db 18 TGCAGGAGCGGAT 5

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DEFINITION AR344603
ACCESSION AR344603
VERSION AR344603.1 GI:33740672
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
          Connors,T.D., Burn,T.C. and Splawski,I.
TITLE Diagnostic method for KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6582913-A 79 24-JUN-2003;
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Best Local Similarity 92.9%; Pred. No. 5.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 TCGAGGAGCGGCT 20
Db 18 TGCAGGAGCGGAT 5
RESULT 22
LOCUS CQ623374 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8114 from Patent WO0192524.
ACCESSION CQ623374
VERSION CQ623374.1 GI:41673592
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8114 06-DEC-2001; Aeomica, Inc. (US)
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      /organism="Homo sapiens"
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Query Match 61.0%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TCTTGCAGGAGCGGCT 20
Db 1 TCTTGCAGGAGCGGCT 17
RESULT 23
LOCUS AR464437 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8114 from patent US '686188.
ACCESSION AR464437
VERSION AR464437.1 GI:42699494
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 686188-A 8114 03-FEB-2004;
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      /note="PCR primer"
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Best Local Similarity 82.4%; Pred. No. 7.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ACTCTTGCAGGAGCGG 18
Db 17 ATTCTTGCAGGAGCGG 1
RESULT 24
LOCUS AX039777 18 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 166 from Patent WO0063441.
ACCESSION AX039777
VERSION AX039777.1 GI:11229806
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Herrnstadt, C. and Davis, R.E.
TITLE Single nucleotide polymorphisms in mitochondrial genes that segregate with alzheimer's disease
JOURNAL Patent: WO 0063441-A 166 26-OCT-2000; MITOKOR (US)
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      /note="PCR primer"
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Best Local Similarity 82.4%; Pred. No. 7.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ACTCTTGCAGGAGCGG 18
Db 17 ATTCTTGCAGGAGCGG 1
RESULT 25
LOCUS AX130162 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1380 from Patent WO030362.
ACCESSION AX130162
VERSION AX130162.1 GI:14136467
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 030362-A 1380 03-MAY-2001; IMMUSOL, INC. (US)
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 18 ACTCTTCTAGAGCGG 2
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RESULT 26
LOCUS      AX674695                17 bp    DNA                linear    PAT 27-MAR-2003
DEFINITION Sequence 3140 from Patent WO03004526.
ACCESSION  AX674695
VERSION     AX674695.1  GI:29333043
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Telerman,A., Amson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL    Patent: WO 03004526-A 3140 16-JAN-2003;
            Molecular Engines Laboratories (FR)
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            /mol_type="unassigned DNA"
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Query Match      60.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  TCTTGCAGGAAG 15
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Db       3  TCTTGCAGGAAG 14

RESULT 27
LOCUS      AX728763/c              17 bp    DNA                linear    PAT 08-MAY-2003
DEFINITION Sequence 397 from Patent WO03025175.
ACCESSION  AX728763
VERSION     AX728763.1  GI:30508106
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Telerman,A., Amson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025175-A 397 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   source
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QY      2  ACTCTTGCAGGA 13
        |||||
Db       14 ACTCTTGCAGGA 3

RESULT 28
LOCUS      AR296765/c              20 bp    DNA                linear    PAT 12-JUN-2003
DEFINITION Sequence 8500 from patent US 6537751.
ACCESSION  AR296765
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VERSION     AR296765.1  GI:31684049
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL    Patent: US 6537751-A 8500 25-MAR-2003;
            Location/Qualifiers
FEATURES   source
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            /organism="unknown"
            /mol_type="genomic DNA"
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Query Match      60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 9.2e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1  GACTCTTGCAGGAAGCGGCT 20
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Db       20 GACTTTTGCACCTAAGCAGAT 1

RESULT 29
LOCUS      BD259354                17 bp    DNA                linear    PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD259354
VERSION     BD259354.1  GI:33069124
KEYWORDS   JP 2002541795-A/7147.
SOURCE     unidentified
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE      Regulation of repressor genes using nucleic acid molecules
JOURNAL    Patent: JP 2002541795-A 7147 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT    OS Eukaryote
            PN JP 2002541795-A/7147
            PD 10-DEC-2002
            PF 11-APR-2000 JP 2000611654
            PR 12-APR-1999 US 60/129390
            PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
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            PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC A61K37/02,
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QY      1  GACTCTTGCAGGAAG 15
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Db       3  GACTATTTCAGGAAG 17
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| Matches               | 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  |
| QY                    | 1 GACTCTTGCAGGAAG 15   |
| Db                    | 1 GACTATTTCAGGAAG 15   |
| RESULT 32             |  |
| AX214649/c            |  |
| LOCUS                 | AX214649 17 bp RNA linear PAT 07-SEP-2001  |
| DEFINITION            | Sequence 91 from Patent WO0159103.   |
| ACCESSION             | AX214649   |
| VERSION               | AX214649.1 GI:15524692   |
| KEYWORDS              | synthetic construct  |
| SOURCE                | synthetic construct  |
| ORGANISM              | other sequences; artificial sequences.   |
| REFERENCE             | 1 Blatt,L., Mcswiggen,J. and Chowrira,B.M.   |
| AUTHORS               | Method and reagent for the modulation and diagnosis of cd20 and  |
| TITLE                 | nogo gene expression   |
| JOURNAL               | Patent: WO 0159103-A 91 16-AUG-2001;<br>RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;<br>McSwiggen, James (US) ; Chowrira, Bharat M. (US)   |
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| Matches               | 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  |
| QY                    | 6 TTGCAGGAAGCGCT 20  |
| Db                    | 16 TTGAAAGAGCGCT 2   |
| RESULT 33             |  |
| AX214650/c            |  |
| LOCUS                 | AX214650 17 bp RNA linear PAT 07-SEP-2001  |
| DEFINITION            | Sequence 92 from Patent WO0159103.   |
| ACCESSION             | AX214650   |
| VERSION               | AX214650.1 GI:15524693   |
| KEYWORDS              | synthetic construct  |
| SOURCE                | synthetic construct  |
| ORGANISM              | other sequences; artificial sequences.   |
| REFERENCE             | 1 Blatt,L., Mcswiggen,J. and Chowrira,B.M.   |
| AUTHORS               | Method and reagent for the modulation and diagnosis of cd20 and  |
| TITLE                 |  |

nogo gene expression  
Patent: WO 0159103-A 92 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McSwiggen, James (US); Chowrira, Bharat M. (US)

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Qy 6 TTGCAGGAAGCGGCT 20  
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RESULT 34  
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LOCUS AX215555 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 997 from Patent WO0159103.  
ACCESSION AX215555  
VERSION AX215555.1 GI:15525598

KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
1

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
JOURNAL nogo gene expression  
Patent: WO 0159103-A 997 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McSwiggen, James (US); Chowrira, Bharat M. (US)

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Db 17 TTGAAGAAGCGGCT 3

RESULT 35  
AX648385/c  
LOCUS AX648385 17 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 225 from Patent EP1273660.  
ACCESSION AX648385  
VERSION AX648385.1 GI:29151203

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1  
AUTHORS Gu, Y.  
TITLE Human sodium-hydrogen exchanger like protein 1  
JOURNAL Patent: EP 1273660-A 225 08-JAN-2003;  
Aeomica, Inc. (US)

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Db 17 TCATGCAAGAAGCGG 3

RESULT 36  
AX648386/c  
LOCUS AX648386 17 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 226 from Patent EP1273660.  
ACCESSION AX648386  
VERSION AX648386.1 GI:29151204

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1  
AUTHORS Gu, Y.  
TITLE Human sodium-hydrogen exchanger like protein 1  
JOURNAL Patent: EP 1273660-A 226 08-JAN-2003;  
Aeomica, Inc. (US)

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Db 16 TCATGCAAGAAGCGG 2

RESULT 37  
AX648387/c  
LOCUS AX648387 17 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 227 from Patent EP1273660.  
ACCESSION AX648387  
VERSION AX648387.1 GI:29151205

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1  
AUTHORS Gu, Y.  
TITLE Human sodium-hydrogen exchanger like protein 1  
JOURNAL Patent: EP 1273660-A 227 08-JAN-2003;  
Aeomica, Inc. (US)

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/mol\_type="unassigned DNA"  
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## ORIGIN

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Qy 4 TCTTGCAGGAGCGG 18
Db 15 TCATGCAAGAAGCGG 1

RESULT 38
LOCUS AR162450/c
DEFINITION Sequence 130 from patent US 6258600.
ACCESSION AR162450
VERSION AR162450.1 GI:16229633
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zhang,H. and Cowseert,L.M.
TITLE Antisense modulation of caspase 8 expression
JOURNAL Patent: US 6258600-A 130 10-JUL-2001;
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Qy 1 GACTCTTGCAGGAG 15
Db 15 GAGTCTTGAAGGAG 1

RESULT 39
LOCUS AX116615/c
DEFINITION Sequence 1738 from Patent WO0129262.
ACCESSION AX116615
VERSION AX116615.1 GI:14033557
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1738 26-APR-2001;
JOURNAL Orchid BioSciences, Inc. (US)
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    Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CTCCTTGCAGGAGCGCT 20
Db 19 CCCATGCAGGTAGTGCT 2

RESULT 40
LOCUS AR067594/c
DEFINITION Sequence 1 from patent US 5851769.
ACCESSION AR067594
VERSION AR067594.1 GI:5998816
KEYWORDS
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gray,J.W. and Weier,H.-U.G.
TITLE Quantitative DNA fiber mapping
JOURNAL Patent: US 5851769-A 1 22-DEC-1998;
FEATURES
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Qy 1 GACTCTTGCAGGAGCGG 18
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OM nucleic - nucleic search, using sw model

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Title: US-10-773-678-342  
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Listing first 100 summaries

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SUMMARIES

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| 3          | 12.8  | 64.0        | 20     | 4  | US-09-081-385-134   |
| 4          | 12.4  | 62.0        | 20     | 1  | US-08-171-718-77    |
| 5          | 12.4  | 62.0        | 20     | 3  | US-08-478-087-77    |
| 6          | 12.4  | 62.0        | 20     | 3  | US-09-135-020-79    |
| 7          | 12.4  | 62.0        | 20     | 3  | US-09-135-010A-79   |
| 8          | 12.4  | 62.0        | 20     | 3  | US-09-444-871-79    |
| 9          | 12.4  | 62.0        | 20     | 3  | US-09-597-735-79    |
| 10         | 12.4  | 62.0        | 20     | 3  | US-09-444-295-79    |
| 11         | 12.4  | 62.0        | 20     | 3  | US-09-597-732-79    |
| 12         | 12.4  | 62.0        | 20     | 4  | US-09-597-731-79    |
| 13         | 12.2  | 61.0        | 17     | 4  | US-09-866-108A-8114 |
| 14         | 12.2  | 61.0        | 19     | 4  | US-09-696-791-1380  |
| 15         | 12    | 60.0        | 20     | 4  | US-09-422-978-8500  |
| 16         | 11.8  | 59.0        | 20     | 3  | US-09-487-445-130   |
| 17         | 11.6  | 58.0        | 20     | 2  | US-08-534-479-1     |
| 18         | 11.6  | 58.0        | 20     | 3  | US-09-489-869-49    |
| 19         | 11.6  | 58.0        | 20     | 4  | US-09-596-248D-38   |
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| 21         | 11.6  | 58.0        | 20     | 4  | US-09-972-115A-29   |
| 22         | 11.4  | 57.0        | 17     | 4  | US-09-866-108A-115  |
| 23         | 11.4  | 57.0        | 17     | 4  | US-09-866-108A-116  |
| 24         | 11.4  | 57.0        | 17     | 4  | US-09-866-108A-117  |
| 25         | 11.4  | 57.0        | 17     | 4  | US-09-866-108A-118  |
| 26         | 11.4  | 57.0        | 17     | 4  | US-09-866-108A-119  |
| 27         | 11.4  | 57.0        | 17     | 4  | US-09-866-108A-6215 |

|    |                     |    |      |      |       |                   |
|----|---------------------|----|------|------|-------|-------------------|
| 4  | US-09-866-108A-6215 | 17 | 57.0 | 11.4 | c 28  | Sequence 6216, Ap |
| 4  | US-09-866-108A-6217 | 17 | 57.0 | 11.4 | c 29  | Sequence 6217, Ap |
| 4  | US-09-866-108A-6218 | 17 | 57.0 | 11.4 | c 30  | Sequence 6218, Ap |
| 17 | US-09-866-108A-6219 | 17 | 57.0 | 11.4 | c 31  | Sequence 6219, Ap |
| 18 | US-09-256-496-10    | 17 | 57.0 | 11.4 | c 32  | Sequence 10, Appl |
| 20 | US-09-517-584A-11   | 17 | 57.0 | 11.4 | c 33  | Sequence 11, Appl |
| 20 | US-09-467-082-27    | 20 | 57.0 | 11.4 | c 34  | Sequence 27, Appl |
| 20 | US-09-658-687A-51   | 20 | 57.0 | 11.4 | c 35  | Sequence 51, Appl |
| 20 | US-09-198-452A-6247 | 20 | 57.0 | 11.4 | c 36  | Sequence 6247, Ap |
| 16 | US-09-856-662-20    | 16 | 56.0 | 11.2 | c 37  | Sequence 20, Appl |
| 17 | US-09-474-432B-429  | 17 | 56.0 | 11.2 | c 38  | Sequence 429, App |
| 17 | US-09-476-387-428   | 17 | 56.0 | 11.2 | c 39  | Sequence 428, App |
| 17 | US-09-866-108A-7632 | 17 | 56.0 | 11.2 | c 40  | Sequence 7632, Ap |
| 17 | US-09-866-108A-7633 | 17 | 56.0 | 11.2 | c 41  | Sequence 7633, Ap |
| 17 | US-09-866-108A-8113 | 17 | 56.0 | 11.2 | c 42  | Sequence 8113, Ap |
| 17 | US-09-866-108A-8115 | 17 | 56.0 | 11.2 | c 43  | Sequence 8115, Ap |
| 19 | US-09-696-791-1379  | 19 | 56.0 | 11.2 | c 44  | Sequence 1379, Ap |
| 20 | US-09-428-583-39    | 20 | 56.0 | 11.2 | c 45  | Sequence 39, Appl |
| 20 | US-07-977-284A-82   | 20 | 55.0 | 11   | c 46  | Sequence 82, Appl |
| 20 | US-08-256-426B-82   | 20 | 55.0 | 11   | c 47  | Sequence 82, Appl |
| 20 | US-09-954-560-16    | 20 | 55.0 | 11   | c 48  | Sequence 16, Appl |
| 20 | US-10-029-517-97    | 20 | 55.0 | 11   | c 49  | Sequence 97, Appl |
| 20 | US-09-232-785-386   | 20 | 55.0 | 11   | c 50  | Sequence 386, App |
| 15 | US-08-311-760A-57   | 15 | 54.0 | 10.8 | c 51  | Sequence 57, Appl |
| 15 | US-08-311-760A-193  | 15 | 54.0 | 10.8 | c 52  | Sequence 193, App |
| 15 | US-08-774-310-57    | 15 | 54.0 | 10.8 | c 53  | Sequence 57, Appl |
| 15 | US-08-774-310-193   | 15 | 54.0 | 10.8 | c 54  | Sequence 193, App |
| 15 | US-09-474-432B-142  | 15 | 54.0 | 10.8 | c 55  | Sequence 142, App |
| 15 | US-09-476-387-142   | 15 | 54.0 | 10.8 | c 56  | Sequence 142, App |
| 17 | US-08-985-162-485   | 17 | 54.0 | 10.8 | c 57  | Sequence 216, App |
| 17 | US-08-985-162-485   | 17 | 54.0 | 10.8 | c 58  | Sequence 485, App |
| 17 | US-09-371-772B-484  | 17 | 54.0 | 10.8 | c 59  | Sequence 484, App |
| 17 | US-09-371-772B-4578 | 17 | 54.0 | 10.8 | c 60  | Sequence 4578, Ap |
| 17 | US-09-476-387-483   | 17 | 54.0 | 10.8 | c 61  | Sequence 483, App |
| 17 | US-09-401-063-216   | 17 | 54.0 | 10.8 | c 62  | Sequence 216, App |
| 17 | US-09-401-063-485   | 17 | 54.0 | 10.8 | c 63  | Sequence 485, App |
| 17 | US-09-866-108A-7634 | 17 | 54.0 | 10.8 | c 64  | Sequence 7634, Ap |
| 17 | US-09-866-108A-7635 | 17 | 54.0 | 10.8 | c 65  | Sequence 7635, Ap |
| 17 | US-09-866-108A-8116 | 17 | 54.0 | 10.8 | c 66  | Sequence 8116, Ap |
| 17 | US-09-866-108A-8117 | 17 | 54.0 | 10.8 | c 67  | Sequence 8117, Ap |
| 18 | US-09-877-177A-1    | 18 | 54.0 | 10.8 | c 68  | Sequence 1, Appl  |
| 18 | US-09-663-834A-47   | 18 | 54.0 | 10.8 | c 69  | Sequence 47, Appl |
| 19 | US-09-676-610B-18   | 19 | 54.0 | 10.8 | c 70  | Sequence 18, Appl |
| 19 | US-09-696-791-3517  | 19 | 54.0 | 10.8 | c 71  | Sequence 3517, Ap |
| 19 | US-09-696-791-3518  | 19 | 54.0 | 10.8 | c 72  | Sequence 3518, Ap |
| 20 | US-08-809-297-39    | 20 | 54.0 | 10.8 | c 73  | Sequence 39, Appl |
| 20 | US-09-226-012-30    | 20 | 54.0 | 10.8 | c 74  | Sequence 30, Appl |
| 20 | US-09-487-368A-93   | 20 | 54.0 | 10.8 | c 75  | Sequence 93, Appl |
| 20 | US-09-489-868A-35   | 20 | 54.0 | 10.8 | c 76  | Sequence 35, Appl |
| 20 | US-09-702-251-44    | 20 | 54.0 | 10.8 | c 77  | Sequence 44, Appl |
| 20 | US-09-844-634-173   | 20 | 54.0 | 10.8 | c 78  | Sequence 173, App |
| 20 | US-09-629-644A-93   | 20 | 54.0 | 10.8 | c 79  | Sequence 93, Appl |
| 20 | US-09-595-684B-18   | 20 | 54.0 | 10.8 | c 80  | Sequence 18, Appl |
| 20 | US-09-198-452A-1521 | 20 | 54.0 | 10.8 | c 81  | Sequence 1521, Ap |
| 20 | US-09-629-644A-93   | 20 | 54.0 | 10.8 | c 82  | Sequence 93, Appl |
| 20 | US-10-177-573-25    | 20 | 54.0 | 10.8 | c 83  | Sequence 25, Appl |
| 17 | US-08-679-645-821   | 17 | 53.0 | 10.6 | c 84  | Sequence 821, App |
| 17 | US-09-866-108A-6214 | 17 | 53.0 | 10.6 | c 85  | Sequence 6214, Ap |
| 17 | US-09-866-108A-7631 | 17 | 53.0 | 10.6 | c 86  | Sequence 7631, Ap |
| 17 | US-09-866-108A-8112 | 17 | 53.0 | 10.6 | c 87  | Sequence 8112, Ap |
| 19 | US-09-747-391-210   | 19 | 53.0 | 10.6 | c 88  | Sequence 210, App |
| 20 | US-07-940-242A-12   | 20 | 53.0 | 10.6 | c 89  | Sequence 12, Appl |
| 20 | US-08-157-235-9     | 20 | 53.0 | 10.6 | c 90  | Sequence 9, Appl  |
| 20 | US-08-244-1183-25   | 20 | 53.0 | 10.6 | c 91  | Sequence 25, Appl |
| 20 | US-08-832-172-3     | 20 | 53.0 | 10.6 | c 92  | Sequence 3, Appl  |
| 20 | US-08-242-580-3     | 20 | 53.0 | 10.6 | c 93  | Sequence 3, Appl  |
| 20 | US-08-470-426B-6    | 20 | 53.0 | 10.6 | c 94  | Sequence 6, Appl  |
| 20 | US-08-337-925-3     | 20 | 53.0 | 10.6 | c 95  | Sequence 3, Appl  |
| 20 | US-09-167-921-29    | 20 | 53.0 | 10.6 | c 96  | Sequence 29, Appl |
| 20 | US-08-647-924-44    | 20 | 53.0 | 10.6 | c 97  | Sequence 44, Appl |
| 20 | US-09-323-743-29    | 20 | 53.0 | 10.6 | c 98  | Sequence 29, Appl |
| 20 | US-09-216-393B-161  | 20 | 53.0 | 10.6 | c 99  | Sequence 161, App |
| 20 |                     | 20 | 53.0 | 10.6 | c 100 |                   |

## ALIGNMENTS

## RESULT 1

US-09-288-461-19  
; Sequence 19, Application US/09288461  
; Patent No. 6159694  
; GENERAL INFORMATION:  
; APPLICANT: Karras, James G.  
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3  
; FILE REFERENCE: ISPH-0338  
; CURRENT APPLICATION NUMBER: US/09/288,461  
; CURRENT FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-288-461-19

Query Match 70.0%; Score 14; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAA 14  
|||||  
DB 7 GACTCTTCAGGAA 20

## RESULT 2

US-09-758-881-19  
; Sequence 19, Application US/09758881  
; Patent No. 6727064  
; GENERAL INFORMATION:  
; APPLICANT: Karras, James G  
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3  
; FILE REFERENCE: ISPH-0532  
; CURRENT APPLICATION NUMBER: US/09/758,881  
; CURRENT FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09054  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 09/288,461  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-758-881-19

Query Match 70.0%; Score 14; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAA 14  
|||||  
DB 7 GACTCTTCAGGAA 20

## RESULT 3

US-09-081-385-134  
; Sequence 134, Application US/09081385  
; Patent No. 6593456

; GENERAL INFORMATION:  
; APPLICANT: Gatanaga, T.  
; APPLICANT: Granger, G.A.  
; TITLE OF INVENTION: Factors Altering Tumor Necrosis  
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods  
; NUMBER OF SEQUENCES: 154  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,385  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/964,747  
; FILING DATE: 05-NOV-1997  
; APPLICATION NUMBER: 60/030,761  
; FILING DATE: 06-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wu, Frank  
; REGISTRATION NUMBER: 41,386  
; REFERENCE/DOCKET NUMBER: 22000-20577.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 134:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-081-385-134

Query Match 64.0%; Score 12.8; DB 4; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGCGC 19  
|||||  
DB 1 TCTTCCAGGAAGCTGC 16

## RESULT 4

US-08-171-718-77/c  
; Sequence 77, Application US/08171718  
; Patent No. 5707863  
; GENERAL INFORMATION:  
; APPLICANT: Trofatter, James A.  
; APPLICANT: MacCollin, Mia M.  
; APPLICANT: Gusella, James F.  
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171,718  
FILING DATE: 22-DEC-1993  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/108,808  
FILING DATE: 19-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/022,034  
FILING DATE: 25-FEB-1993  
APPLICATION NUMBER: US 08/026,063  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Anne  
REGISTRATION NUMBER: 36,463  
REFERENCE/DOCKET NUMBER: 0609.3850003  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-171-718-77

Query Match 62.0%; Score 12.4; DB 1; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTCCTGCAGGAGC 16  
Db 15 CTCCTGCAGGTAGC 2

RESULT 5  
US-08-478-087-77/c  
Sequence 77, Application US/08478087  
Patent No. 6077685  
GENERAL INFORMATION:  
APPLICANT: Trofatter, James A.  
APPLICANT: MacCollin, Mia M.  
APPLICANT: Gusella, James F.  
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,087  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/171,718  
FILING DATE: 22-DEC-1993  
APPLICATION NUMBER: US 08/108,808  
FILING DATE: 19-AUG-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/022,034  
FILING DATE: 25-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/026,063  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Anne  
REGISTRATION NUMBER: 36,463  
REFERENCE/DOCKET NUMBER: 0609.3850003  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-478-087-77

Query Match 62.0%; Score 12.4; DB 3; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTCCTGCAGGAGC 16  
Db 15 CTCCTGCAGGTAGC 2

RESULT 6  
US-09-135-020-79/c  
Sequence 79, Application US/09135020  
Patent No. 6274332  
GENERAL INFORMATION:  
APPLICANT: Keating, Mark T.  
APPLICANT: Sanguinetti, Michael C.  
APPLICANT: Spawlski, Igor  
TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH  
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING  
TITLE OF INVENTION: KCNE1 AS AN LQT GENE  
FILE REFERENCE: 2323-131  
CURRENT APPLICATION NUMBER: US/09/135,020  
CURRENT FILING DATE: 1998-08-17  
EARLIER APPLICATION NUMBER: 08/921,068  
EARLIER FILING DATE: 1997-08-29  
EARLIER APPLICATION NUMBER: 08/739,383  
EARLIER FILING DATE: 1996-10-29  
EARLIER APPLICATION NUMBER: 60/019,014  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 60/094,477  
EARLIER FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 79  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-135-020-79

Query Match 62.0%; Score 12.4; DB 3; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCCAGGAGCGGCT 20  
Db 18 TCCAGGAGCGGAT 5

RESULT 7  
US-09-135-010A-79/c  
Sequence 79, Application US/09135010A  
Patent No. 6277978  
GENERAL INFORMATION:

; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Curran, Mark E.  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Connors, Timothy D.  
; APPLICANT: Burn, Timothy C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE  
; FILE REFERENCE: 2323-133  
; CURRENT APPLICATION NUMBER: US/09/135,010A  
; CURRENT FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 60/094,477  
; PRIOR FILING DATE: 1998-07-29  
; PRIOR APPLICATION NUMBER: 08/921,068  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 79  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-135-010A-79

Query Match 62.0%; Score 12.4; DB 3; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGCT 20  
| | | | | | | | | | | | | | | | | | | | | |  
DB 18 TGCAGGAAGCGGAT 5

RESULT 8  
US-09-444-871-79/c  
; Sequence 79, Application US/09444871  
; Patent No. 6323026  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH  
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING  
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE  
; FILE REFERENCE: 2323-131  
; CURRENT APPLICATION NUMBER: US/09/444,871  
; CURRENT FILING DATE: 1999-11-22  
; EARLIER APPLICATION NUMBER: US/09/135,020  
; EARLIER FILING DATE: 1998-08-17  
; EARLIER APPLICATION NUMBER: 08/921,068  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER APPLICATION NUMBER: 08/739,383  
; EARLIER FILING DATE: 1996-10-29  
; EARLIER APPLICATION NUMBER: 60/019,014  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 60/094,477  
; EARLIER FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 79  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-444-871-79

Query Match 62.0%; Score 12.4; DB 3; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGCT 20

Db 18 TGCAGGAAGCGGAT 5  
| | | | | | | | | | | | | | | | | | | | | |  
RESULT 9  
US-09-597-735-79/c  
; Sequence 79, Application US/09597735  
; Patent No. 6420124  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Curran, Mark E.  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Connors, Timothy D.  
; APPLICANT: Burn, Timothy C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE  
; FILE REFERENCE: 2323-133  
; CURRENT APPLICATION NUMBER: US/09/597,735  
; CURRENT FILING DATE: 2000-06-19  
; EARLIER APPLICATION NUMBER: 09/135,010  
; EARLIER FILING DATE: 1998-08-17  
; EARLIER APPLICATION NUMBER: 60/094,477  
; EARLIER FILING DATE: 1998-07-29  
; EARLIER APPLICATION NUMBER: 08/921,068  
; EARLIER FILING DATE: 1997-08-29  
; EARLIER APPLICATION NUMBER: 08/739,383  
; EARLIER FILING DATE: 1996-10-29  
; EARLIER APPLICATION NUMBER: 60/019,014  
; EARLIER FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 79  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-597-735-79

Query Match 62.0%; Score 12.4; DB 3; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGCT 20  
| | | | | | | | | | | | | | | | | | | | | |  
DB 18 TGCAGGAAGCGGAT 5

RESULT 10  
US-09-444-295-79/c  
; Sequence 79, Application US/09444295  
; Patent No. 6432844  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH  
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING  
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE  
; FILE REFERENCE: 2323-131  
; CURRENT APPLICATION NUMBER: US/09/444,295  
; CURRENT FILING DATE: 1999-11-22  
; PRIOR APPLICATION NUMBER: 09/135,020  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 08/921,068  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; PRIOR APPLICATION NUMBER: 60/094,477  
; PRIOR FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 79  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-444-295-79

Query Match 62.0%; Score 12.4; DB 3; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGCT 20  
||| ||||| |||||  
Db 18 TGCAGGAAGCGGAT 5

## RESULT 11

US-09-597-732-79/c  
; Sequence 79, Application US/09597732  
; Patent No. 6451534  
; GENERAL INFORMATION:

; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Curran, Mark E.  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Connors, Timothy D.  
; APPLICANT: Burn, Timothy C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE

; FILE REFERENCE: 2323-133  
; CURRENT APPLICATION NUMBER: US/09/597,732  
; CURRENT FILING DATE: 2000-06-19

; PRIOR APPLICATION NUMBER: 09/135,010  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 60/094,477  
; PRIOR FILING DATE: 1998-07-29  
; PRIOR APPLICATION NUMBER: 08/921,068  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 79  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-597-732-79

Query Match 62.0%; Score 12.4; DB 3; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGCT 20  
||| ||||| |||||  
Db 18 TGCAGGAAGCGGAT 5

## RESULT 12

US-09-597-731-79/c  
; Sequence 79, Application US/09597731  
; Patent No. 6582913  
; GENERAL INFORMATION:

; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Curran, Mark E.  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Connors, Timothy D.  
; APPLICANT: Burn, Timothy C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE

; FILE REFERENCE: 2323-133  
; CURRENT APPLICATION NUMBER: US/09/597,731

; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 09/135,010  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 08/921,068  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 79  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-597-731-79

Query Match 62.0%; Score 12.4; DB 4; Length 20;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGCT 20  
||| ||||| |||||  
Db 18 TGCAGGAAGCGGAT 5

## RESULT 13

US-09-866-108A-8114  
; Sequence 8114, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEWICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: AEWICA Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 8114  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-8114

Query Match 61.0%; Score 12.2; DB 4; Length 17;

Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGCT 20  
Db 1 TCCTGCCAGGAAGCGGCT 17

RESULT 14  
US-09-696-791-1380/c  
; Sequence 1380, Application US/09696791  
; Patent No. 6770633  
; GENERAL INFORMATION:  
; APPLICANT: Robbins, Joan M.  
; APPLICANT: Tritz, Richard  
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: SKIN AND EYE DISEASES  
; FILE REFERENCE: 480124.407  
; CURRENT APPLICATION NUMBER: US/09/696,791  
; CURRENT FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 4523  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1380  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Cdk-we-hu ribozyme binding site  
US-09-696-791-1380

Query Match 61.0%; Score 12.2; DB 4; Length 19;  
Best Local Similarity 82.4%; Pred. No. 7.5e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGG 18  
Db 18 ACTCTTCTAGAGCGG 2

RESULT 15  
US-09-422-978-8500/c  
; Sequence 8500, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 8500  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..20  
; OTHER INFORMATION: downstream amplification primer 99-15968 for SEQ 635, in complete  
US-09-422-978-8500

Query Match 60.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 75.0%; Pred. No. 9.6e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAAGGCGCT 20

Db 20 GACTTTTGCACTAAGCAGAT 1

RESULT 16  
US-09-487-445-130/c  
; Sequence 130, Application US/09487445  
; Patent No. 6258600  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION  
; FILE REFERENCE: RTS-0107  
; CURRENT APPLICATION NUMBER: US/09/487,445  
; CURRENT FILING DATE: 2000-01-19  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 130  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-487-445-130

Query Match 59.0%; Score 11.8; DB 3; Length 20;  
Best Local Similarity 86.7%; Pred. No. 1.2e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAAGGAG 15  
Db 15 GAGTCTTGGAAGGAG 1

RESULT 17  
US-08-534-479-1/c  
; Sequence 1, Application US/08534479  
; Patent No. 5851769  
; GENERAL INFORMATION:  
; APPLICANT: GRAY, JOE W.  
; APPLICANT: WEIER, HEINZ-ULRICH G.  
; TITLE OF INVENTION: QUANTITATIVE FIBER MAPPING  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/534,479  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MACKNIGHT, KAMRIN T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: LBL-01754  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-534-479-1

```
Query Match          58.0%; Score 11.6; DB 2; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCGAGGAGCGG 18
   ||| ||||| |||
DB 20 GAGTACTGCGAGGAGG 3

RESULT 18
US-09-489-869-49/c
; Sequence 49, Application US/09489869A
; Patent No. 6268151
; GENERAL INFORMATION:
; APPLICANT: Susan Murray
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MACROPHAGE MIGRATION INHIBITORY FACTOR
; FILE REFERENCE: RTS-0110
; CURRENT APPLICATION NUMBER: US/09/489,869A
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-489-869-49

Query Match          58.0%; Score 11.6; DB 3; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CTCCTTCGAGGAGCGGCT 20
   ||| ||||| |||
DB 18 CTCCTACAGCAAGTGCT 1

RESULT 19
US-09-596-248D-38/c
; Sequence 38, Application US/09596248D
; Patent No. 6599727
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J
; APPLICANT: Goldman, Phyllis S
; APPLICANT: McElligott, David L
; TITLE OF INVENTION: Human Poly(ADP-Ribose) Polymerase 2 Materials and
; FILE REFERENCE: Methods
; CURRENT APPLICATION NUMBER: US/09/596,248D
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/139,543
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-596-248D-38

Query Match          58.0%; Score 11.6; DB 4; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCGAGGAGCGG 18
   ||| ||||| |||
DB 19 GGCCTCTTGGTGGAGCGG 2
```

```
RESULT 20
US-09-596-248D-39
; Sequence 39, Application US/09596248D
; Patent No. 6599727
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J
; APPLICANT: Goldman, Phyllis S
; APPLICANT: McElligott, David L
; TITLE OF INVENTION: Human Poly(ADP-Ribose) Polymerase 2 Materials and
; FILE REFERENCE: Methods
; CURRENT APPLICATION NUMBER: US/09/596,248D
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/139,543
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-596-248D-39

Query Match          58.0%; Score 11.6; DB 4; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCGAGGAGCGG 18
   ||| ||||| |||
DB 2 GGCCTCTTGGTGGAGCGG 19

RESULT 21
US-09-972-115A-29
; Sequence 29, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-972-115A-29

Query Match          58.0%; Score 11.6; DB 4; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCGAGGAGCGG 18
   ||| ||||| |||
DB 3 GACAATTGCTGGAAGCTG 20
```

```

RESULT 22
US-09-866-108A-115
; Sequence 115, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 115
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-115

Query Match          57.0%; Score 11.4; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TCTTGCAGGAAGC 16
      ||| |||||
DB      5 TCTGGCAGGAAGC 17

RESULT 23
US-09-866-108A-116
; Sequence 116, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 116
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-116

Query Match          57.0%; Score 11.4; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TCTTGCAGGAAGC 16
      ||| |||||
DB      5 TCTGGCAGGAAGC 17

RESULT 24
US-09-866-108A-117
; Sequence 117, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 117
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-117

Query Match          57.0%; Score 11.4; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TCTTGCAGGAAGC 16
      ||| |||||
DB      4 TCTGGCAGGAAGC 16

```

; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 117  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-117

Query Match 57.0%; Score 11.4; DB 4; Length 17;  
Best Local Similarity 92.3%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGC 16  
||| |||||  
Db 3 TCTGGCAGGAAGC 15

## RESULT 25

US-09-866-108A-118  
; Sequence 118, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US 60/207,456  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 118  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-118

Query Match 57.0%; Score 11.4; DB 4; Length 17;  
Best Local Similarity 92.3%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGC 16  
||| |||||  
Db 2 TCTGGCAGGAAGC 14

RESULT 26  
US-09-866-108A-119  
; Sequence 119, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 119  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-119

Query Match 57.0%; Score 11.4; DB 4; Length 17;  
Best Local Similarity 92.3%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGC 16  
||| |||||  
Db 1 TCTGGCAGGAAGC 13

## RESULT 27

US-09-866-108A-6215/c  
; Sequence 6215, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456

Qy 4 TCTTGCAGGAAGC 16  
||| |||||  
Db 1 TCTGGCAGGAAGC 13

```
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6215
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6215

Query Match          57.0%; Score 11.4; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GACTCTTGCAGGA 13
      ||||| |||||
Db      17 GACTCTTGCAGGA 5

RESULT 28
US-09-866-108A-6216/c
; Sequence 6216, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6217
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6217

Query Match          57.0%; Score 11.4; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GACTCTTGCAGGA 13
      ||||| |||||
Db      17 GACTCTTGCAGGA 5

RESULT 28
US-09-866-108A-6216/c
; Sequence 6216, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6217
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6217
```

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; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6216
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6216

Query Match          57.0%; Score 11.4; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GACTCTTGCAGGA 13
      ||||| |||||
Db      16 GACTCTTGCAGGA 4

RESULT 29
US-09-866-108A-6217/c
; Sequence 6217, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6217
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6217

Query Match          57.0%; Score 11.4; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GACTCTTGCAGGA 13
      ||||| |||||
Db      15 GACTCTTGCAGGA 3
```

```

RESULT 30
US-09-866-108A-6218/c
; Sequence 6218, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 6218
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-6218

Query Match 57.0%; Score 11.4; DB 4; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGA 13
Db 14 GACTGTTGCAGGA 2

RESULT 31
US-09-866-108A-6219/c
; Sequence 6219, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25

```

```
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF E2F TRANSCRIPTION FACTOR 1 EXPRESSION
; FILE REFERENCE: RTS-0121
; CURRENT APPLICATION NUMBER: US/09/517,584A
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-584A-11

Query Match 57.0%; Score 11.4; DB 3; Length 20;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTGCAGGAGCGG 18
DB 13 TTGCAGGAGCGG 1

RESULT 34
US-09-467-082-27
; Sequence 27, Application US/09467082
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0088
; CURRENT APPLICATION NUMBER: US/09/467,082
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-082-27

Query Match 57.0%; Score 11.4; DB 3; Length 20;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CTTCGAGGAGCG 17
DB 2 CTTCGAGGATGCG 14

RESULT 35
US-09-658-687A-51
; Sequence 51, Application US/09658687A
; Patent No. 6387699
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
; FILE REFERENCE: RTS-0141
; CURRENT APPLICATION NUMBER: US/09/658,687A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-687A-51

Query Match 57.0%; Score 11.4; DB 3; Length 20;
```

```
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAGC 16
DB 2 TCTTGCAGGAGC 14
```

```
RESULT 36
US-09-198-452A-6247
; Sequence 6247, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6247
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6247
```

```
Query Match 57.0%; Score 11.4; DB 4; Length 20;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTCTTGCGAGGAG 15
DB 5 CTATTGCGAGGAG 17
```

```
RESULT 37
US-09-856-662-20/C
; Sequence 20, Application US/09856662
; Patent No. 6790616
; GENERAL INFORMATION:
; APPLICANT: MORIBE, Toyoki et al.
; TITLE OF INVENTION: Method for typing HLA class 1 genes
; FILE REFERENCE: 0032-0261P
; CURRENT APPLICATION NUMBER: US/09/856,662
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: JP P1998-335151
; PRIOR FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA probe A402G
US-09-856-662-20
```

```
Query Match 56.0%; Score 11.2; DB 4; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACTCTTGCGAGGAGCG 17
DB 16 ACCCGCGCGAGGAGCG 1
```

```
RESULT 38
US-09-474-432B-429
; Sequence 429, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

APPLICANT: Beigelman, Leo  
APPLICANT: Burgin, Alex  
APPLICANT: Beaudry, Amber  
APPLICANT: Karpeisky, Alex  
APPLICANT: Adamic, Jasenka  
APPLICANT: Sweedler, David  
APPLICANT: Zinnen, Shawn  
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot  
FILE REFERENCE: MBH00-831-B (247/276)  
CURRENT APPLICATION NUMBER: US/09/474,432B  
CURRENT FILING DATE: 1999-12-19  
PRIOR APPLICATION NUMBER: US 60/064,866  
PRIOR FILING DATE: 1997-11-05  
PRIOR APPLICATION NUMBER: US 60/084,727  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: US 09/186,675  
PRIOR FILING DATE: 1998-11-04  
PRIOR APPLICATION NUMBER: US 09/301,511  
PRIOR FILING DATE: 1999-04-28  
NUMBER OF SEQ ID NOS: 1526  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 429  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-474-432B-429

Query Match 56.0%; Score 11.2; DB 4; Length 17;  
Best Local Similarity 68.8%; Pred. No. 2.4e+04;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCGAGGAC 16  
Db 2 GACUGCUGCAGGAAC 17

RESULT 39  
US-09-476-387-428  
Sequence 428, Application US/09476387  
Patent No. 6617438  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Beigelman, Leo  
APPLICANT: Beaudry, Amber  
APPLICANT: Karpeisky, Alex  
APPLICANT: Adamic, Jasenka Matulic  
APPLICANT: Sweedler, Dave  
APPLICANT: Zinnen, Shawn  
TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot  
FILE REFERENCE: MBH00-831-C (249/073)  
CURRENT APPLICATION NUMBER: US/09/476,387  
CURRENT FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 09/474,432  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/301,511  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: 09/186,675  
PRIOR FILING DATE: 1998-11-04  
PRIOR APPLICATION NUMBER: 60/083,727  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/064,866  
PRIOR FILING DATE: 1997-11-05  
NUMBER OF SEQ ID NOS: 1524  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 428  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-476-387-428

Query Match 56.0%; Score 11.2; DB 4; Length 17;  
Best Local Similarity 68.8%; Pred. No. 2.4e+04;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCGAGGAC 16  
Db 2 GACUGCUGCAGGAAC 17

RESULT 40  
US-09-866-108A-7632/c  
Sequence 7632, Application US/09866108A  
Patent No. 6686188  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharron G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/006666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006655  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/006663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15755  
SOFTWARE: Aecomica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 7632  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-7632

Query Match 56.0%; Score 11.2; DB 4; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.4e+04;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTGCGAGGAGCG 18  
Db 17 CTCTAGCAGGACGAG 2

Search completed: August 6, 2005, 16:30:01  
Job time : 92 secs

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 09:48:11 ; Search time 231 Seconds  
(without alignments)  
512.532 Million cell updates/sec

Title: US-10-773-678-342

Perfect score: 20

Sequence: 1 gactcttcaggaagcgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2207178

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N\_Geneseq\_16Dec04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description        |
|------------|-------|---------------|--------|----|--------------------|
| 1          | 14    | 70.0          | 20     | 3  | AAC93168 Human STA |
| 2          | 14    | 70.0          | 20     | 6  | AAS96785 Human STA |
| 3          | 13.6  | 68.0          | 20     | 12 | ADM14825 Human mPG |
| 4          | 13    | 65.0          | 15     | 4  | AAP46591 IGFBP3 ol |
| 5          | 13    | 65.0          | 15     | 4  | AAP46590 IGFBP3 ol |
| 6          | 13    | 65.0          | 15     | 4  | AAP46589 IGFBP3 ol |
| 7          | 12.6  | 63.0          | 20     | 12 | ADM92376 Pancreat  |
| 8          | 12.6  | 63.0          | 20     | 12 | ADM14384 Human mPG |
| 9          | 12.6  | 63.0          | 20     | 12 | ADM14826 Human mPG |
| 10         | 12.4  | 62.0          | 17     | 10 | ADB45311 Tumour su |
| 11         | 12.4  | 62.0          | 17     | 10 | ACC52408 Human tum |
| 12         | 12.4  | 62.0          | 18     | 12 | AAS39770 SNP speci |
| 13         | 12.4  | 62.0          | 18     | 12 | ADB34379 Reverse p |
| 14         | 12.4  | 62.0          | 20     | 2  | AAQ71136 Merlin ex |
| 15         | 12.4  | 62.0          | 20     | 2  | AAT90721 Human KVL |
| 16         | 12.4  | 62.0          | 20     | 2  | AAT91069 Human KVL |
| 17         | 12.4  | 62.0          | 20     | 3  | AAZ90745 Human KVL |
| 18         | 12.4  | 62.0          | 20     | 3  | AAZ98975 Mutant hu |
| 19         | 12.4  | 62.0          | 20     | 13 | ADR72365 Antisense |
| 20         | 12.4  | 62.0          | 20     | 13 | ADR72397 Antisense |

|    |      |      |    |    |          |                    |
|----|------|------|----|----|----------|--------------------|
| 21 | 12.2 | 61.0 | 17 | 6  | ABN08122 | Abn08122 Human GDM |
| 22 | 12.2 | 61.0 | 17 | 13 | ACN71212 | Acn71212 Human GDM |
| 23 | 12.2 | 61.0 | 18 | 3  | AAC67455 | Aac67455 Alzheimer |
| 24 | 12.2 | 61.0 | 19 | 3  | AAA83794 | Aaa83794 cdk-we-hu |
| 25 | 12.2 | 61.0 | 19 | 5  | AAH58956 | Aah58956 Cdk-we-hu |
| 26 | 12.2 | 61.0 | 19 | 13 | ADT01798 | Adt01798 Novel mut |
| 27 | 12.2 | 61.0 | 20 | 2  | AAT89003 | Aat89003 Human mas |
| 28 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 29 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 30 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 31 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 32 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 33 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 34 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 35 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 36 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 37 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 38 | 12.2 | 61.0 | 20 | 2  | AAZ02042 | Aaz02042 PCR prime |
| 39 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 40 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 41 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 42 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 43 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 44 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 45 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 46 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 47 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 48 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 49 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 50 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 51 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 52 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 53 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 54 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 55 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 56 | 11.8 | 59.0 | 20 | 12 | ADM14320 | Adm14320 Human mPG |
| 57 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 58 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 59 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 60 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 61 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 62 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 63 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 64 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 65 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 66 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 67 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 68 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 69 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 70 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 71 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 72 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 73 | 11.6 | 58.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 74 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 75 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 76 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 77 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 78 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 79 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 80 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 81 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 82 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 83 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 84 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 85 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 86 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 87 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 88 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 89 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 90 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 91 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 92 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |
| 93 | 11.4 | 57.0 | 20 | 12 | ADJ61051 | Adj61051 Oligonuc  |

c 94 11.4 57.0 17 13 ACN69314 Human GDM  
95 11.4 57.0 17 13 ACN63214 Human GDM  
96 11.4 57.0 18 3 AAX57670 Human G-a  
97 11.4 57.0 20 2 AAX96921 PCR prime  
c 98 11.4 57.0 20 3 AAC72420 Single nu  
99 11.4 57.0 20 4 AAC72420 Primer fo  
c 100 11.4 57.0 20 4 AAF91296 Human E2F

## ALIGNMENTS

RESULT 1  
AAC93168  
ID AAC93168 standard; DNA; 20 BP.  
XX  
AC AAC93168;  
XX  
DT 15-FEB-2001 (first entry)  
XX  
DE Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:19.  
XX  
KW Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide;  
KW modulation; signal transducer and activator of transcription;  
KW DNA-binding protein; signal transduction; inhibition; apoptosis;  
KW inflammatory disease; cancer; antinflammatory; antirheumatic;  
KW cytosolic; immunostimulatory; rheumatoid arthritis; leukaemia; myeloma;  
KW melanoma; lymphoma; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200061602-A1.  
XX  
PD 19-OCT-2000.  
XX  
PF 06-APR-2000; 2000WO-US009054.  
XX  
PR 08-APR-1999; 99US-00288461.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Karras JG;  
XX  
DR WPI; 2000-619223/59.  
XX  
PS New antisense compound for inhibiting the expression of signal transducer  
CC and activator of transcription 3 (STAT3) in cells or tissues and treating  
CC diseases or condition associated with STAT3, such as rheumatoid arthritis  
CC and cancer.  
XX  
PT Example 2; Page 46; 104pp; English.

XX  
PS The present invention describes an antisense compound (I), 8 to 30  
CC nucleobases in length, that is targeted to a nucleic acid molecule  
CC encoding STAT3 (Signal Transducer and Activator of Transcription) and  
CC which inhibits the expression of it. (I) has antinflammatory,  
CC antirheumatic, cytostatic and immunostimulatory activities. (I) is used  
CC for inhibiting the expression of STAT3 in cells or tissues, treating an  
CC animal having a disease or condition associated with STAT3 or a human  
CC having a disease or condition characterised by a reduction in apoptosis,  
CC and inducing apoptosis in a cell. Diseases or conditions that are treated  
CC are rheumatoid arthritis, cancer of the breast, prostate, brain, head  
CC and/or neck, leukaemia, myeloma, melanoma or lymphoma. (I) can also be  
CC used for diagnostic methods in detecting and determining the role of  
CC STAT3 in various cell functions, physiological processes and conditions.  
CC and for diagnosing the conditions associated with expression of STAT3.  
CC (I) can be used alone or with other drugs as an immunostimulator. (I) is  
CC used in sandwich and colourimetric assays, involving enzyme conjugation  
CC and radiolabeling and is used in diagnostic kits. AAC93150 encodes human  
CC STAT3 and AAC93231 encodes mouse STAT3 as given in the exemplification of  
CC the present invention. AAC93151 to AAC93230 and AAC93232 to AAC93299  
CC represent STAT3 phosphorothioate antisense oligonucleotides, and AAC93300  
CC represents a mismatch control oligonucleotide which are used in example

CC from the present invention  
XX  
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 70.0%; Score 14; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GACTCTTGCAGGAA 14  
|||||||  
Db 7 GACTCTTGCAGGAA 20  
RESULT 2  
AAS96785  
ID AAS96785 standard; DNA; 20 BP.  
XX  
AC AAS96785;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DE Human STAT3 antisense phosphorothioate oligodeoxynucleotide #18.  
XX  
KW STAT3; human; signal transducer and activator of transcription; ss; STAT;  
KW antisense gene therapy; Fas-mediated apoptosis; inflammatory disease;  
KW autoimmune disease; rheumatoid arthritis; cancer; breast; prostate; head;  
KW neck; brain; leukaemia; myeloma; melanoma; lymphoma; apoptosis;  
KW antinflammatory; immunosuppressive; antirheumatic; antiarthritic;  
KW cytosolic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FN US2001029250-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 11-JAN-2001; 2001US-00758881.  
XX  
PR 08-APR-1999; 99US-00288461.  
PR 06-APR-2000; 2000WO-US009054.  
XX  
PA (KARR/) KARRAS J G.  
XX  
PI Karras JG;  
XX  
DR WPI; 2002-009991/01.  
XX  
PT Novel antisense compound useful for treating and diagnosing inflammatory  
PT diseases and cancers, is targeted to a nucleic acid molecule encoding  
PT signal transducer and activator of transcription proteins.  
XX  
PS Example 2; Page 13; 21pp; English.  
XX  
CC The invention relates to antisense compounds targeted to a nucleic acid  
CC molecule encoding a signal transducer and activator of transcription  
CC (STAT) protein, specifically STAT3, where the antisense compounds inhibit  
CC the expression of STAT3. The antisense sequences are useful for  
CC inhibiting the expression of STAT3 in cells or tissues, inducing Fas-  
CC mediated apoptosis in cells, and sensitising cells to apoptosis. They are  
CC also useful for treating an animal having a disease or condition  
CC associated with STAT3. These disorders include inflammatory or autoimmune  
CC disease, particularly rheumatoid arthritis, cancers, such as those of the  
CC breast, prostate, brain and head and neck and leukaemias, myelomas,  
CC melanomas and lymphomas. Also treatable are human diseases or conditions  
CC characterised by a reduction in apoptosis or an insensitivity to  
CC apoptotic signals. The sequences of the invention can be used in clinical  
CC research, for detecting and determining the role of STAT3 in various cell  
CC functions and physiological processes and for diagnosing conditions  
CC associated with the expression of STAT3. The sequences represent cDNA  
XX encoding human STAT3 and human STAT3 oligonucleotides  
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;





CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 65.0%; Score 13; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 GCAGGAAGCGGCT 20  
DB 15 GCAGGAAGCGGCT 3  
  
RESULT 7  
ADM92376/c  
ID ADM92376 standard; DNA; 20 BP.  
XX  
AC  
XX ADM92376;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Pancreatic cancer related RT-PCR forward primer SEQ ID NO:13.  
XX  
KW pancreatic cancer; diagnosis; pancreatic cancer-associated gene;  
KW cytotatic; vaccine; gene therapy; human; reverse transcription; PCR;  
KW primer; ss; semi-quantitative RT-PCR experiment.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO2004031412-A2.  
XX  
PD 15-APR-2004.  
XX  
XX  
PF 17-SEP-2003; 2003WO-JP011817.  
XX  
PR 30-SEP-2002; 2002US-0414872P.  
PR 28-FEB-2003; 2003US-0450889P.  
XX  
XX (ONCO-) ONCOTHERAPY SCI INC.  
PA (UYTY) UNIV TOKYO.  
XX  
XX Nakamura Y, Katagiri T;  
XX  
XX WPI; 2004-330205/30.  
XX  
XX  
PT Diagnosing pancreatic cancer (PNC) comprises determining a level of  
PT expression of a PNC-associated gene in a patient derived biological  
PT sample.  
XX  
XX Example 1; SEQ ID NO 13; 152pp; English.  
XX  
XX The present invention describes a method for diagnosing pancreatic cancer  
CC (PNC) or a predisposition to developing PNC in a subject. The method  
CC comprises determining a level of expression of a PNC-associated gene in a  
CC patient derived biological sample, where an increase or decrease of the  
CC level compared to a normal control level of the gene indicates that the  
CC subject suffers from or is at risk of developing PNC. Also described: (1)  
CC a PNC reference expression profile, comprising a pattern of gene  
CC expression of two or more genes, i.e. PNC 1-605 or PNC 850-866 and PNC  
CC 894-906; (2) a method of screening for a compound for treating or  
CC preventing PNC or malignant PNC; (3) a kit comprising a detection reagent  
CC which binds to two or more nucleic acid sequences, i.e. PNC 1-605 or PNC  
CC 850-866 and PNC 894-906 or the encoded polypeptides; (4) an array  
CC comprising two or more nucleic acids which bind to one or more nucleic  
CC acid sequences, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906; (5) a  
CC method of treating or preventing PNC in a subject; (6) a composition, for  
CC treating or preventing PNC, comprising a pharmaceutical amount of: (a) an  
CC antisense polynucleotide or small interfering RNA against a  
CC polynucleotide, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-  
CC 933; (b) an antibody or antibody fragment that binds to a protein encoded  
CC by any one gene, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-

CC 893; or (c) the compound obtained by the method of (2) as an active  
CC ingredient and a pharmaceutical carrier; and (7) a method of predicting  
CC recurrence of PNC. The compounds have cytostatic activity, and can be  
CC used in vaccines and in gene therapy. The method is useful in diagnosing  
CC PNC or a predisposition to developing PNC in a subject. The methods, the  
CC compounds and compositions are useful in treating or preventing PNC. The  
CC polypeptides are useful as vaccines against PNC. The present sequence  
CC represents a reverse transcription (RT) PCR primer used in semi-  
CC quantitative RT-PCR experiments related to the diagnosis of PNC, which is  
CC used in an example from the present invention.  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 63.0%; Score 12.6; DB 12; Length 20;  
Best Local Similarity 78.9%; Pred. No. 2.6e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 ACTCTTGACGAGGCGCT 20  
DB 20 AATCTCCAGGAGCTGCT 2  
  
RESULT 8  
ADM14384/c  
ID ADM14384 standard; DNA; 20 BP.  
XX  
AC  
XX ADM14384;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:571.  
XX  
KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytotatic; antidiabetic;  
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20 /\*tag= b  
FT /\*mod\_base= OTHER  
FT /\*note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5 /\*tag= a  
FT /\*mod\_base= OTHER  
FT /\*note= "2'-O-methoxyethyls"  
FT modified\_base 16..20 /\*tag= c  
FT /\*mod\_base= OTHER  
FT /\*note= "2'-O-methoxyethyls"  
XX WO2004028458-A2.  
XX  
XX 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030374.  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
XX (PMDA ) PHARMACIA CORP.  
XX  
XX Gierse JK;  
XX WPI; 2004-305094/28.  
DR

XX New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 PT ischemia.  
 XX  
 PS Claim 4; SEQ ID NO 571; 132pp; English.  
 XX  
 CC The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to  
 CC 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytostatic,  
 CC antidiabetic, immunomodulator, cardiant, neuroprotective,  
 CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX  
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 63.0%; Score 12.6; DB 12; Length 20;  
 Best Local Similarity 78.9%; Pred. No. 2.6e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GACTCTTGACGAGCGGC 19  
 DB 19 GATTCTGCACGAGTGCC 1  
 RESULT 9  
 ADM14826/c  
 ID ADM14826 standard; DNA; 20 BP.  
 XX  
 AC ADM14826;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1013.  
 XX  
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;  
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxycethyls"  
 FT modified\_base 16..20  
 FT /\*tag= c

FT  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxycethyls"  
 XX  
 FN W02004028458-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PP 25-SEP-2003; 2003WO-US030374.  
 XX  
 PR 25-SEP-2002; 2002US-0413549P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Gierse JK;  
 XX  
 DR WPI; 2004-305094/28.  
 XX  
 PT New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 PT ischemia.  
 XX  
 PS Claim 4; SEQ ID NO 1013; 132pp; English.  
 XX  
 CC The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to  
 CC 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytostatic,  
 CC antidiabetic, immunomodulator, cardiant, neuroprotective,  
 CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX  
 SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 63.0%; Score 12.6; DB 12; Length 20;  
 Best Local Similarity 78.9%; Pred. No. 2.6e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 ACTCTTGACGAGCGGCT 20  
 DB 20 ATTCTGCGACGAGTGCT 2  
 RESULT 10  
 ADB45311  
 ID ADB45311 standard; DNA; 17 BP.  
 XX  
 AC ADB45311;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Tumour suppression/reversion associated nucleotide #5634.  
 XX  
 KW cytostatic; antiviral; neuroprotective; neurotropic; neuroleptic; ss;  
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FN W02003040369-A2.  
 XX

```
PD 15-MAY-2003.
XX
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX
DR WPI; 2003-441574/41.
XX
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX
PS Disclosure; Page 690; 771pp; French.
XX
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX
SQ Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 10; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTTCAGGAGCG 17
| | | | | | | | |
DB 3 TCTTCAGGAGAG 16

RESULT 11
ACCS2408
ID ACC52408 standard; DNA; 17 BP.
XX
XX
AC ACC52408;
XX
XX
DT 27-JUN-2003 (first entry)
XX
XX
DE Human tumour suppressor sequence #1175.
XX
XX
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
XX
OS Homo sapiens.
XX
XX
PN FR2826373-A1.
XX
XX
PD 27-DEC-2002.
XX
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
XX
PR 20-JUN-2001; 2001FR-00008139.

(MOLE-) MOLECULAR ENGINES LAB SA.
Tuijnder M, Telerman A, Amson R;
WPI; 2003-250498/25.

New nucleic acid sequences associated with tumor suppression, regression,
apoptosis or virus resistance are useful to diagnose and treat viral
disease, development of tumor cells and cell degeneration.

Claim 1; Page 311; 798pp; French.

This sequence represents an isolated nucleic acid sequence associated
with tumour suppression or regression, apoptosis or virus resistance. The
invention relates to these sequences or sequences having at least 80%
identity to them, and polypeptides encoded by the sequences or
polypeptides having 80% identity to the polypeptide sequences. The
invention is used to diagnose or treat viral disease or disease
characterized by development of tumour cells or cellular degeneration

Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 10; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TCCAGGAAGCGGCT 20
| | | | | | | | |
DB 3 TCCAGGAAGCGGCT 16

RESULT 12
AAH39770
ID AAH39770 standard; DNA; 18 BP.
XX
XX
AC AAH39770;
XX
XX
DT 14-AUG-2001 (first entry)
XX
XX
DE SNP specific lower PCR primer SEQ ID 2566.
XX
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200129262-A2.
XX
XX
PD 26-APR-2001.
XX
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
XX
PR 15-OCT-1999; 99US-0160096P.
XX
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX
PI Picoult-Newburg L, Pohl M;
XX
XX
DR WPI; 2001-290930/30.
XX
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX
PS Claim 1; Page 63; 83pp; English.
XX
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
```

CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence

XX Sequence 18 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 62.0%; Score 12.4; DB 4; Length 18;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTGCGAGGAGCGG 18  
 Db 3 CTGCGAGGAGCGG 16

RESULT 13  
 ADE34379  
 ID ADE34379 standard; DNA; 18 BP.

AC ADE34379;

29-JAN-2004 (first entry)

Reverse primer P4.

XX Helicobacter pylori; gastric carcinoma; Lewis antigen; polymorphism; PCR;  
 KW primer; ss.

OS Unidentified.

XX WO2003080840-A1.

PD 02-OCT-2003.

PF 26-MAR-2002; 2002WO-CN000199.

PR 26-MAR-2002; 2002WO-CN000199.

PA (UYPE-) UNIV PEKING SCHOOL ONCOLOGY.

PI Ke Y, Jiang J, Ning T, Lu G, You W, Pan K;

XX WPI; 2004-011526/01.

XX Inspecting genetic susceptibility of Helicobacter pylori- related gastric  
 PT carcinoma by checking Lewis blood-type antigen-associated gene  
 PT polymorphism, applicable in screening individuals with high risk.

PS Example 2; Page 14; 37pp; Chinese.

XX The invention relates to a method for inspecting the genetic  
 CC susceptibility of Helicobacter pylori related gastric carcinoma. The  
 CC method of the invention comprises checking the polymorphism of the Lewis  
 CC blood-type antigen-associated gene, with susceptibility particularly  
 CC based on the recessive se allele and/or dominant homozygous Se/Se

CC genotype. The method is applicable in screening individuals with high  
 CC risk and in a follow-up survey for intervention, prevention and early  
 CC diagnosis. In an experiment from the invention the Lewis gene fragments  
 CC with T59G, G508A and T1067A polymorphism sites for PCR amplification were  
 CC obtained for use after extracting samples of peripheral lymphocyte DNA  
 CC from subjects. The mutation was then identified for assessing disease  
 CC risk and diagnosis. The current sequence represents a PCR primer for  
 CC amplification of a region of the Lewis gene.

XX Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 12; Length 18;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACTCTTCGAGGAG 15

Db 3 ACTCTTCGAGGAG 16

RESULT 14  
 AAQ71136/c  
 ID AAQ71136 standard; cDNA; 20 BP.

AC AAQ71136;

XX 25-MAR-2003 (revised)

DT 20-APR-1995 (first entry)

XX Merlin exon 10 primer #1, amplifies 260 bp product.

XX Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
 KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
 KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;  
 KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
 KW merlin-associated tumour; D22S1; posterior capsular lens opacity;  
 KW deafness; balance disorder; paralysis; ss.

XX Synthetic.

XX EP613945-A2.

XX 07-SEP-1994.

XX 25-FEB-1994; 94EP-00301367.

XX 25-FEB-1993; 93US-00022034.

PR 04-MAR-1993; 93US-00026063.

PR 19-AUG-1993; 93US-00108808.

PR 22-DEC-1993; 93US-00171718.

XX (GEHO ) GEN HOSPITAL CORP.

PI Trofatter JA, Maccollin NM, Gusella JF;

XX WPI; 1994-272992/34.

XX The tumour suppressor gene merlin - for treatment and diagnosis of  
 PT tumours and neurofibromatosis (NF2).

PS Example 6; Page 27; 86pp; English.

XX The sequences given in AAQ71110-55 are primers which were used to amplify  
 CC the 17 exons of the NF2 gene. NF2 is a neurofibromatosis which is  
 CC characterised by bi-lateral schwannomas. The NF2 "gene" has been shown by  
 CC linkage studies to be assigned to chromosome 22. The missing or mutated  
 CC gene in NF2 patients has been shown to be the merlin gene. The gene  
 CC encodes a protein, merlin (moesin-erzin-radixin-like protein), which  
 CC possesses tumour suppressor activity, and whose tumour suppressor  
 CC activity is mediated by interactions with the cytoskeleton. The merlin  
 CC gene is found on chromosome 22 between the known markers D22S1 and  
 CC D22S28. In patients suffering from NF2, the merlin gene is either lost or  
 CC mutated. A mutant merlin protein may be encoded by a gene in which a

CC mutation of A to T at the first position of the codon encoding amino acid  
 CC 220 causes the substitution of Tyr for Asn. The merlin gene may be used  
 CC in gene therapy for the treatment of a merlin-associated tumour or NF2,  
 CC or for prevention of schwannoma, meningioma, posterior capsular lens  
 CC opacities, deafness or hearing loss, balance disorders or paralysis.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ

Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 2; Length 20;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CTCCTGCAGGAGC 16  
 Db 15 CTCCTGCAGGTAGC 2

## RESULT 15

AAT90721/c  
 ID AAT90721 standard; cDNA; 20 BP.

XX AAT90721;

XX 12-FEB-1998 (first entry)

XX Human KVLQT1 S4 region PCR primer 5.

XX KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel; diagnosis;  
 KW therapy; human; single strand conformation polymorphism; primer; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9723598-A2.

XX 03-JUL-1997.

XX 20-DEC-1996; 96WO-US019756.

XX 22-DEC-1995; 95US-0019014P.

XX 29-OCT-1996; 96US-00739383.

XX (UTAH) UNIV UTAH RES FOUND.

XX Keating MT, Sanguinetti MC, Curran ME;

XX WPI; 1997-402190/37.

XX Human minK and Xenopus KVLQT1 coding sequences - used for assays for  
 PT identifying drugs which can be used for preventing or treating long QT  
 PT syndrome.

XX Example 12; Page 44; 105pp; English.

XX PCR primer 5 (AAT90721) and primer 6 (AAT90722) were designed to amplify  
 CC DNA encoding the S4 region of human KVLQT1 (see AAW30038). PCR primers  
 CC (AAT90717-28) were used in single-strand conformation analysis (SSCP) to  
 CC define mutations in the human KVLQT1 gene (see AAT90730) associated with  
 CC long QT syndrome (LQT). An initial SSCP identified an anomalous conformer  
 CC in LQT-affected members of 6 large families. Further SSCP analyses  
 CC identified a KVLQT1 intragenic deletion and 9 missense mutations  
 CC associated with LQT in small families and sporadic cases

XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 2; Length 20;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAGCGGCT 20  
 Db 18 TGCAGGAGCGGAT 5

## RESULT 16

AAT91069/c

ID AAT91069 standard; DNA; 20 BP.

XX AAT91069;

XX 01-MAR-1998 (first entry)

XX Human KVLQT1 S4 region PCR primer 5.

XX KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel; diagnosis;  
 KW therapy; human; PCR; primer; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9723632-A1.

XX 03-JUL-1997.

XX 20-DEC-1996; 96WO-US019917.

XX 22-DEC-1995; 95US-0019014P.

XX 29-OCT-1996; 96US-00739383.

XX (UTAH) UNIV UTAH RES FOUND.

XX (GENZ) GENZYME GENETICS.

XX Keating MF, Curran ME, Landes GM, Connors TD;

XX WPI; 1997-402191/37.

XX New isolated human potassium channel gene, KVLQT1, - used to develop

XX products for diagnosis, prevention and therapy of long QT syndrome.

XX Example 12; Page 44; 105pp; English.

XX PCR primer 5 (AAT91069) and primer 6 (AAT91070) were designed to amplify  
 CC DNA encoding the S4 region of human KVLQT1 (see AAW33355). PCR primers  
 CC (AAT91065-76) were used in single-strand conformation analysis (SSCP) to  
 CC define mutations in the human KVLQT1 gene (see AAT94004) associated with  
 CC long QT syndrome (LQT). An initial SSCP identified an anomalous conformer  
 CC in LQT-affected members of 6 large families. Further SSCP analyses  
 CC identified a KVLQT1 intragenic deletion and 9 missense mutations  
 CC associated with LQT in small families and sporadic cases

XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 2; Length 20;  
 Best Local Similarity 92.9%; Pred. No. 3.3e+04;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAGCGGCT 20  
 Db 18 TGCAGGAGCGGAT 5

## RESULT 17

AAZ90745/c

ID AAZ90745 standard; DNA; 20 BP.

XX AAZ90745;

XX 19-JUN-2000 (first entry)

XX Human KVLQT1 mutation defining primer 5.

XX KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;  
 KW antiarrhythmic; gene therapy; human; PCR primer; ss.

XX Homo sapiens.

```
XX PN WO200006600-A1.
XX PD 10-FEB-2000.
XX PF 06-OCT-1998; 98WO-US017838.
XX PR 29-JUL-1998; 98US-0094477P.
XX PR 17-AUG-1998; 98US-00135020.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Keating MT, Sanguinetti MC, Splawski I;
XX WPI; 2000-195262/17.
XX DR
XX PT Mutant forms of genes encoding mink protein and KVLQT1 protein involved
XX PT in cardiac potassium channel formation useful for screening drugs, for
XX PT preventing and treating cardiac arrhythmia.
XX PS Example 13; Page 75; 167pp; English.
XX CC The invention relates to KVLQT1 and KCNE1 genes, associated with long QT
XX CC (LQT) syndrome. It provides a mink protein comprising a mutation which
XX CC substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and
XX CC Ala or Thr at residues 74, 76, 28, 32, 98 and 127 respectively. Screening
XX CC KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and
XX CC treating LQT. The ability to predict LQT enables physicians to prevent
XX CC the diseases with medical therapy such as beta blocking agents and opts
XX CC for better treatments. Sequences AAZ90741-290752 represent PCR primers
XX CC for defining human KVLQT1 mutations
XX SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGCT 20
Db 18 TGCAGGAAGCGGAT 5

RESULT 18
AAZ98975/c
ID AAZ98975 standard; DNA; 20 BP.
AC AAZ98975;
XX
XX 06-JUN-2000 (first entry)
XX DE Mutant human long QT syndrome-associated KVLQT1 diagnostic primer 5.
XX KW KVLQT1; mutation; human; cardiac I (ks) potassium channel; KCNE1; ss;
XX KW cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy;
XX KW chromosome 11p15.5; PCR primer.
XX OS Homo sapiens.
XX OS WO200006199-A1.
XX PN
XX PD 10-FEB-2000.
XX PF 12-MAY-1999; 99WO-US010260.
XX PR 29-JUL-1998; 98US-0094477P.
XX PR 17-AUG-1998; 98US-00135010.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PA (GENZ ) GENZYME CORP.
XX PI Keating MT, Sanguinetti MC, Curran ME, Landes GM, Connors TD;
XX PI Burn TC, Splawski I;
```

```
XX DR WPI; 2000-195199/17.
XX PT New isolated mutant KVLQT1 nucleic acids, useful for developing products
XX PT for the diagnosis, prevention and treatment of long QT syndrome.
XX PS Example 13; Page 78; 178pp; English.
XX CC The invention relates to KVLQT1 nucleic acids which have a mutation
XX CC compared to wild-type KVLQT1 (AAZ98901) The KVLQT1 gene encodes a protein
XX CC of 676 amino acids which forms a cardiac I(ks) potassium channel with the
XX CC KCNE1 protein (AAZ90563). The KVLQT1 gene contains 15 introns and encodes
XX CC a protein containing 6 putative transmembrane segments and a pore forming
XX CC region. The gene has been mapped to the chromosomal location 11p15.5. The
XX CC sequences AAZ98971-298982 represent PCR primers used to diagnose
XX CC mutations in the KVLQT1 gene. Mutations in the KVLQT1 or KCNE1 genes
XX CC result in cardiac arrhythmias observed as a prolonged QT curve in
XX CC electrocardiograms (Long QT syndrome). The genes and proteins can be used
XX CC for the diagnosis of subjects with long QT syndrome. They can also be
XX CC used to screen for drugs which can be used for treating or preventing
XX CC long QT syndrome. The KVLQT1 nucleic acids can be used for gene therapy,
XX CC and KVLQT1 peptides can be used for peptide therapy
XX SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGCT 20
Db 18 TGCAGGAAGCGGAT 5

RESULT 19
ADR72365/c
ID ADR72365 standard; DNA; 20 BP.
XX
XX ADR72365;
AC ADR72365;
XX
XX 02-DEC-2004 (first entry)
XX DE Antisense oligo targeted to human kinesin-like 1, ISIS 344901.
XX KW Antisense; kinesin-like 1; N2 kinesin; bimC kinesin;
XX KW cellular proliferation; cancer; B-cell leukaemia; autoimmune disease;
XX KW carpal tunnel syndrome; Raynaud's phenomenon; systemic sclerosis;
XX KW Sjorgren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis;
XX KW systemic lupus erythematosus; human; ss; ISIS 344901; rat.
XX OS Homo sapiens.
XX OS Rattus sp.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate nucleotide. All cytosines
XX FT are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are
XX FT 2'-methoxyethyl nucleotides."
XX PN
XX PD US2004180847-A1.
XX PF 16-SEP-2004.
XX PR 17-NOV-2003; 2003US-00714796.
XX PR 23-MAY-2002; 2002US-00156603.
XX PA (DOBI/) DOBIE K W.
XX PA (KOLL/) KOLLER E.
XX
```

PI Dobie KW, Koller E;  
XX WPI; 2004-652550/63.  
XX  
XX New antisense compound 8 to 80 nucleobases in length targeted to a  
PT nucleic acid molecule encoding kinesin-like 1, useful for treating an  
PT animal having a disease or condition such as cancer, tumor, autoimmune  
PT disease.  
XX  
XX Example 30; SEQ ID NO 129; 110pp; English.  
PS  
XX The present invention relates to antisense compounds, compositions and  
CC methods for modulating the expression of kinesin-like 1. The superfamily  
CC of kinesins function as molecular engines to bind and transport vesicles  
CC and organelles along microtubules using energy supplied by ATP. Kinesin-  
CC like 1, a member of the N2 (also called bimC) family of kinesins, is  
CC involved in separating the chromosomes by directing their movement along  
CC microtubules in the bipolar spindle. Kinesin-like 1 is also known as  
CC KNSL1, Eg5, HsEg5, HKSP, KIF11, thyroid interacting protein 5 and TRIP5.  
CC Inhibition of kinesin-like 1 may be a target for arresting cellular  
CC proliferation in cancer, due to its central role in mitosis. Expression  
CC of kinesin-like 1 expression may contribute to other disease states such  
CC as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome,  
CC Raynaud's phenomenon, systemic sclerosis, Sjogren's syndrome, rheumatoid  
CC arthritis, polymyositis and polyarteritis. Kinesin-like 1 is an  
CC autoantigen identified in systemic lupus erythematosus. The invention  
CC relates to antisense nucleic acid oligomers, targeted to the gene  
CC encoding kinesin-like 1. Also provided are methods of screening for  
CC modulators of kinesin-like 1 and to methods of modulating the expression  
CC of kinesin-like 1. At least a portion of the compound hybridises with RNA  
CC to form an oligonucleotide-RNA duplex. It has at least one modified  
CC internucleoside linkage, sugar moiety, or nucleobase. It has at least one  
CC 2'-O-methoxyethyl sugar moiety, phosphorothioate internucleoside linkage,  
CC or one cytosine which is a 5-methylcytosine. The antisense compound may  
CC comprise an antisense nucleic acid molecule that is specifically  
CC hybridisable with a 5'-untranslated region (UTR), with a start region,  
CC with a coding region, with a 3'-UTR, with an intron, or with an intron-  
CC exon junction of a nucleic acid molecule encoding kinesin-like 1.  
CC Oligonucleotides were synthesised via solid phase P(III) phosphoramidite  
CC chemistry. The present sequence is an antisense oligo targeted to human  
XX kinesin-like 1, ISIS #344902.  
XX  
SQ Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;  
Query Match 62.0%; Score 12.4; DB 13; Length 20;  
Best Local Similarity 92.9%; Pred. No. 3.3e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 TCTTCGAGGAGCG 17  
DB 20 TCTTCGAGGAGTG 7  
RESULT 20  
AD72397/c  
ID AD72397 standard; DNA; 20 BP.  
XX  
XX AD72397;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Antisense oligo targeted to mouse kinesin-like 1, ISIS 285690.  
XX  
XX Antisense; kinesin-like 1; N2 kinesin; bimC kinesin;  
KW cellular proliferation; cancer; B-cell leukaemia; autoimmune disease;  
KW carpal tunnel syndrome; Raynaud's phenomenon; systemic sclerosis;  
KW Sjogren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis;  
KW systemic lupus erythematosus; mouse; ss; human.  
XX  
XX Mus musculus.  
OS Homo sapiens.  
OS Synthetic.

FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /mod\_base= a  
FT /note= "OTHER= phosphorothioate nucleotide. All cytosines  
FT are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are  
FT 2'-methoxyethyl nucleotides."  
XX  
XX US2004180847-A1.  
XX  
XX 16-SEP-2004.  
XX  
XX 17-NOV-2003; 2003US-00714796.  
XX  
XX 23-MAY-2002; 2002US-00156603.  
XX  
XX (DOBI/) DOBIE K W.  
XX (KOLL/) KOLLER E.  
XX  
XX Dobie KW, Koller E;  
XX  
XX WPI; 2004-652550/63.  
XX  
XX New antisense compound 8 to 80 nucleobases in length targeted to a  
PT nucleic acid molecule encoding kinesin-like 1, useful for treating an  
PT animal having a disease or condition such as cancer, tumor, autoimmune  
PT disease.  
XX  
XX Claim 36; SEQ ID NO 161; 110pp; English.  
PS  
XX The present invention relates to antisense compounds, compositions and  
CC methods for modulating the expression of kinesin-like 1. The superfamily  
CC of kinesins function as molecular engines to bind and transport vesicles  
CC and organelles along microtubules using energy supplied by ATP. Kinesin-  
CC like 1, a member of the N2 (also called bimC) family of kinesins, is  
CC involved in separating the chromosomes by directing their movement along  
CC microtubules in the bipolar spindle. Kinesin-like 1 is also known as  
CC KNSL1, Eg5, HsEg5, HKSP, KIF11, thyroid interacting protein 5 and TRIP5.  
CC Inhibition of kinesin-like 1 may be a target for arresting cellular  
CC proliferation in cancer, due to its central role in mitosis. Expression  
CC of kinesin-like 1 expression may contribute to other disease states such  
CC as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome,  
CC Raynaud's phenomenon, systemic sclerosis, Sjogren's syndrome, rheumatoid  
CC arthritis, polymyositis and polyarteritis. Kinesin-like 1 is an  
CC autoantigen identified in systemic lupus erythematosus. The invention  
CC relates to antisense nucleic acid oligomers, targeted to the gene  
CC encoding kinesin-like 1. Also provided are methods of screening for  
CC modulators of kinesin-like 1 and to methods of modulating the expression  
CC of kinesin-like 1. At least a portion of the compound hybridises with RNA  
CC to form an oligonucleotide-RNA duplex. It has at least one modified  
CC internucleoside linkage, sugar moiety, or nucleobase. It has at least one  
CC 2'-O-methoxyethyl sugar moiety, phosphorothioate internucleoside linkage,  
CC or one cytosine which is a 5-methylcytosine. The antisense compound may  
CC comprise an antisense nucleic acid molecule that is specifically  
CC hybridisable with a 5'-untranslated region (UTR), with a start region,  
CC with a coding region, with a 3'-UTR, with an intron, or with an intron-  
CC exon junction of a nucleic acid molecule encoding kinesin-like 1.  
CC Oligonucleotides were synthesised via solid phase P(III) phosphoramidite  
CC chemistry. The present sequence is an antisense oligo targeted to mouse  
XX kinesin-like 1.  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;  
Query Match 62.0%; Score 12.4; DB 13; Length 20;  
Best Local Similarity 92.9%; Pred. No. 3.3e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 TCTTCGAGGAGCG 17  
DB 19 TCTTCGAGGAGTG 6  
RESULT 21

ABN08122  
ID ABN08122 standard; DNA; 17 BP.  
XX AC ABN08122;  
XX DT 29-MAY-2002 (first entry)  
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8114.  
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX OS Homo sapiens.  
XX FN WO200192524-A2.  
XX PD 06-DEC-2001.  
XX PF 25-MAY-2001; 2001WO-US016981.  
XX PR 26-MAY-2000; 2000US-0207456P.  
XX PR 21-SEP-2000; 2000US-0234687P.  
XX PR 27-SEP-2000; 2000US-0236359P.  
XX PR 04-OCT-2000; 2000GB-00024263.  
XX PR 30-JAN-2001; 2001WO-US000661.  
XX PR 30-JAN-2001; 2001WO-US000662.  
XX PR 30-JAN-2001; 2001WO-US000663.  
XX PR 30-JAN-2001; 2001WO-US000664.  
XX PR 30-JAN-2001; 2001WO-US000665.  
XX PR 30-JAN-2001; 2001WO-US000666.  
XX PR 30-JAN-2001; 2001WO-US000667.  
XX PR 30-JAN-2001; 2001WO-US000668.  
XX PR 30-JAN-2001; 2001WO-US000669.  
XX PR 05-FEB-2001; 2001WO-US000670.  
XX PR 05-FEB-2001; 2001US-0266860P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX DR  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 8114; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequence  
XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 6; Length 17;  
Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 4 TCTTGCAGGAAGCGGCT 20  
Db 1 TCTTGCAGGAAGCGGCT 17  
RESULT 22  
ACN71212  
ID ACN71212 standard; DNA; 17 BP.  
XX AC ACN71212;  
XX DT 02-DEC-2004 (first entry)  
XX DE Human GDMPLP-1 probe SEQ ID NO:8114.  
XX KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX OS Homo sapiens.  
XX FN US2004137589-A1.  
XX PD 15-JUL-2004.  
XX PF 26-NOV-2003; 2003US-00723361.  
XX PR 26-MAY-2000; 2000US-0207456P.  
XX PR 21-SEP-2000; 2000US-0234687P.  
XX PR 27-SEP-2000; 2000US-0236359P.  
XX PR 04-OCT-2000; 2000GB-00024263.  
XX PR 30-JAN-2001; 2001WO-US000661.  
XX PR 30-JAN-2001; 2001WO-US000662.  
XX PR 30-JAN-2001; 2001WO-US000663.  
XX PR 30-JAN-2001; 2001WO-US000664.  
XX PR 30-JAN-2001; 2001WO-US000665.  
XX PR 30-JAN-2001; 2001WO-US000666.  
XX PR 30-JAN-2001; 2001WO-US000667.  
XX PR 30-JAN-2001; 2001WO-US000668.  
XX PR 30-JAN-2001; 2001WO-US000669.  
XX PR 05-FEB-2001; 2001WO-US000670.  
XX PR 05-FEB-2001; 2001US-0266860P.  
XX PR 25-MAY-2001; 2001US-00866108.  
XX PA (GUY/) GU Y.  
XX PA (JIY/) JI Y.  
XX PA (PENN/) PENN S G.  
XX PA (HANZ/) HANZEL D K.  
XX PA (RANK/) RANK D.  
XX PA (CHEN/) CHEN W.  
XX PA (SHAN/) SHANNON M E.  
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX WPI; 2004-533378/51.  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
XX function.  
XX Disclosure; SEQ ID NO 8114; Opp; English.  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or

CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103

SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 13; Length 17;  
Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAGCGGCT 20  
DB 1 TCTTGCAGGAGCGGCT 17

RESULT 23  
AAC67455/c  
ID AAC67455 standard; DNA; 18 BP.

XX AAC67455;

XX 14-FEB-2001 (first entry)

DE Alzheimer's disease-linked mitochondrial SNP PCR primer #155.

XX Human; mitochondrial genome; single nucleotide polymorphism; SNP;  
KW Alzheimer's disease; mtDNA; PCR primer; ss.

OS Homo sapiens.

XX WO200063441-A2.

XX 26-OCT-2000.

XX 19-APR-2000; 2000WO-US010906.

XX 20-APR-1999; 99US-0130447P.

XX 22-OCT-1999; 99US-0160901P.

XX (MITO-) MITOKOR.

XX Hernstadt C, Davis RE;

XX WPI; 2000-672748/65.

PT Diagnosing a subject at the risk for or having Alzheimer's disease  
PT comprises determining at least one single nucleotide polymorphism in  
PT mitochondrial DNA associated with the disease in the sample from the  
PT subject.

XX Example 4; Page 41; 89pp; English.

CC The present invention describes a novel method for determining the risk  
CC of or diagnosing Alzheimer's disease using single nucleotide  
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA  
CC (mtDNA). In addition, the SNPs identified can be used to identify agents  
CC suitable for use in treating Alzheimer's disease. Sequences AAC67301-  
CC C67610 are PCR primers used to demonstrate the method of the invention

SQ Sequence 18 BP; 5 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 3; Length 18;  
Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAGCGG 18  
DB 17 ATTCTTGCAGGAGCGG 1

RESULT 24  
AAA83794/c  
ID AAA83794 standard; DNA; 19 BP.

XX AAA83794;

XX 04-DEC-2000 (first entry)

XX cdk-we-hu ribozyme binding site #269.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
XX Mammalia.

XX WO200032765-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US028772.

XX 04-DEC-1998; 98US-0110954P.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
PT PCNA and Cyclin B1.

XX Disclosure; Page 67; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme,  
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
CC Representative examples of ribozyme recognition sites are given in  
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
CC inhibiting restenosis by introduction of the ribozyme into cells. The  
CC ribozyme is resistant to endonuclease activity and hence is efficient in  
CC restenosis treatment

XX Sequence 19 BP; 5 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 3; Length 19;  
Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAGCGG 18  
DB 18 ACTCTTCTAGAGCGG 2

RESULT 25  
AAH58956/c  
ID AAH58956 standard; DNA; 19 BP.

XX AAH58956;

XX 10-SEP-2001 (first entry)

XX Cdk-we-hu ribozyme binding site SEQ ID NO:1380.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
KW recognition site; target; ribozyme binding site; eye disease; vulnary;  
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;  
KW antiskinking; ophthalmological; keratolytic; gene therapy; viral wart;  
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;

KW sickle cell retinopathy; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200130362-A2.  
 XX  
 XX 03-MAY-2001.  
 PD  
 XX 26-OCT-2000; 2000WO-US029500.  
 XX  
 XX 26-OCT-1999; 99US-0161532P.  
 PR  
 XX (IMMU-) IMMUSOL INC.  
 PA  
 XX Robbins JM, Tritz R;  
 PI  
 XX WPI; 2001-300427/31.  
 DR  
 XX  
 XX Treating proliferative skin or eye diseases and scarring, using ribozymes  
 PT that cleave RNA encoding cytokines involved in inflammation, matrix  
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
 XX  
 XX Example 1; Page 172; 408pp; English.  
 PS  
 XX The present invention describes a method for treating a proliferative  
 CC skin or eye disease and scarring. The method involves administering a  
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
 CC dependent kinase, growth factor or a reductase, or administering a  
 CC nucleic acid molecule (II) comprising a promoter operably linked to a  
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,  
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,  
 CC ophthalmological, vulnary, keratolytic and virucide activities, and  
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
 CC also be used for treating proliferative eye diseases such as diabetic  
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
 CC prematurity and retinal detachment, and for treating and preventing  
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
 CC scar. AAH57577 to AAH62099 represent sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 19 BP; 5 A; 4 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 61.0%; Score 12.2; DB 5; Length 19;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 ACTCTTGCAGGAAGCG 18  
 Db 18 ACTCTTCTAGAAGCG 2  
 RESULT 26  
 ADT01798  
 ID ADT01798 standard; DNA; 19 BP.  
 XX  
 AC ADT01798;  
 XX  
 XX 16-DEC-2004 (first entry)  
 DT  
 XX  
 XX Novel mutant protein tyrosine kinase-related oligonucleotide SeqID1786.  
 DE  
 XX tyrosine kinase; cancer; anti-cancer agent; signalling molecule;  
 KW tumorigenesis; somatic alteration; colorectal cancer; NTRK3; FES;  
 KW GUCY2F; MCKK; MLK4; Kinase domain; cytostatic; tyrosine kinase inhibitor;  
 KW guanylate cyclase stimulator; ss.  
 XX  
 XX Homo sapiens.  
 OS

PN WO2004082458-A2.  
 XX  
 PD 30-SEP-2004.  
 XX  
 XX 18-FEB-2004; 2004WO-US004452.  
 PF  
 XX 21-FEB-2003; 2003US-0448537P.  
 PR  
 XX 29-MAY-2003; 2003US-0473895P.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Bardelli A, Parsons W, Velculescu V, Kinzler KW, Vogelstein B;  
 PI  
 XX WPI; 2004-718702/70.  
 DR  
 XX Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCKK) and  
 PT associated methods for diagnosing cancer and screening for anti-cancer  
 PT agents.  
 PT  
 XX Disclosure; SEQ ID NO 1786; 363pp; English.  
 PS  
 XX This invention relates to a novel activated mutant protein tyrosine  
 CC kinases and associated methods for diagnosing cancer and screening for  
 CC anti-cancer agents. Protein kinases are signalling molecules involved in  
 CC tumorigenesis. Mutational analysis of the human tyrosine kinase gene  
 CC family identified somatic alterations in 1 in 5 colorectal cancers, with  
 CC the majority of mutations occurring in the NTRK3, FES, GUCY2F and  
 CC MCKK/MLK4 genes. Most were identified in the kinase domain. The invention  
 CC may be useful for the production of compounds with a cytostatic activity  
 CC acting as protein tyrosine kinase inhibitors or guanylate cyclase  
 CC stimulators. The invention may be useful for developing methods for  
 CC detecting mutations involved in cancer or screening for anti-cancer  
 CC agents. The present sequence is that of a human-derived oligonucleotide  
 CC which is related to the invention.  
 XX  
 SQ Sequence 19 BP; 6 A; 4 C; 7 G; 2 T; 0 U; 0 Other;  
 Query Match 61.0%; Score 12.2; DB 13; Length 19;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GACTCTTGCAGGAAGCG 17  
 Db 3 GACTCTTGCAGGAAGCG 19  
 RESULT 27  
 AAT89003/c  
 ID AAT89003 standard; DNA; 20 BP.  
 XX  
 AC AAT89003;  
 XX  
 XX 22-APR-1998 (first entry)  
 DT  
 XX  
 XX Human maspin Ets wild-type sense oligonucleotide DNA.  
 DE  
 XX Maspin; serpin; mammary epithelial cell; human; promoter; malignant;  
 KW tumour cell; treatment; prostate cancer; breast cancer; metastasis;  
 KW primer; ss.  
 KW  
 XX Synthetic.  
 OS  
 OS Homo sapiens.  
 XX  
 PN WO9736179-A1.  
 XX  
 XX 02-OCT-1997.  
 PD  
 XX 28-MAR-1997; 97WO-US005186.  
 PF  
 XX 28-MAR-1996; 96US-0014368P.  
 PR  
 XX (DAND ) DANA FARBER CANCER INST.  
 PA (PARD/) PARDEE A.

XX Sagar R, Zhang M;  
 XX WPI; 1997-489785/45.  
 XX Maspin gene promoter fragment - used to identify compounds for treatment  
 PT of prostate or breast cancer.  
 XX Disclosure; Page 12; 51pp; English.  
 XX Primers AAT89003-T89008 are used in electrophoretic mobility shift assay  
 CC experiments to analyse the maspin promoter region. AAT89003 is designed  
 CC as a Ets regulatory element wild type (WT) sense oligonucleotide. Maspin  
 CC is a serpin which is expressed in mammary epithelial cells. Its  
 CC expression in these cells decreases with increasing malignancy and is  
 CC lost in during metastasis. Maspin protein is also known to inhibit the  
 CC mobility of tumour cells. This gene can be used in method for screening  
 CC compounds to identify candidate compounds for the treatment of prostate  
 CC cancer, or breast cancer. It can also be used to identify compounds that  
 CC increase the expression of maspin, and for detecting the presence of  
 CC metastatic prostate epithelial cells  
 XX  
 XX Sequence 20 BP; 3 A; 11 C; 3 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 61.0%; Score 12.2; DB 2; Length 20;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 TCTTCAGGAGCGGCT 20  
 DB 18 TCGGGCAGGAGGGGCT 2  
 RESULT 28  
 AAZ02042  
 ID AAZ02042 standard; DNA; 20 BP.  
 XX  
 AC AAZ02042;  
 XX  
 XX 07-OCT-1999 (first entry)  
 XX  
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.  
 XX  
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;  
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;  
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
 KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.  
 XX  
 OS Synthetic.  
 OS Chlamydia trachomatis.  
 XX  
 XX WO9928475-A2.  
 XX  
 XX 10-JUN-1999.  
 XX  
 XX 27-NOV-1998; 98WO-IB001939.  
 XX  
 XX 28-NOV-1997; 97FR-00015041.  
 PR 17-DEC-1997; 97FR-00016034.  
 PR 04-NOV-1998; 98US-0107077P.  
 XX  
 XX (GEST ) GENSET.  
 PA  
 XX Griffais R;  
 PI  
 XX WPI; 1999-371125/31.  
 DR  
 XX Genome sequence of Chlamydia trachomatis.  
 PT  
 XX Disclosure; Page 1492; 1755pp; English.  
 PS  
 XX PCR primers AAZ01426-Z06209 were used to amplify open reading frames  
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs

CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines  
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
 CC be used to control growth of the microorganism. Chlamydia trachomatis is  
 CC responsible for a large number of diseases, e.g. eye diseases such as  
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion  
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;  
 CC epididymitis, cervicitis, salpingitis, perihhepatitis, Bartholinitis;  
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
 CC The polypeptides of the invention may be of use in treating these  
 CC diseases  
 XX  
 XX Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
 SQ

Query Match 61.0%; Score 12.2; DB 2; Length 20;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAGCG 17  
 |||||  
 DB 4 GACTCTTCAGGAGCTCG 20

## RESULT 29

AAAX79782/c  
 ID AAX79782 standard; DNA; 20 BP.

XX AC AAX79782;

XX 17-AUG-1999 (first entry)

XX PCR primer H15340 for mitochondrial DNA analysis.

KW PCR primer; human; mitochondrial DNA; genetic diagnosis;  
 KW adult disease contraction; ss.

XX Synthetic.

OS Homo sapiens.

XX JP111133597-A.

XX 27-APR-1999.

XX 13-OCT-1997; 97JP-00279127.

XX 13-OCT-1997; 97JP-00279127.

XX (TANA/) TANAKA M.

XX WPI; 1999-320841/27.

XX Genetic diagnosis using human mitochondrial DNA - comprises detecting  
 PT base replacements.

XX Example 2; Page 6; 15pp; Japanese.

XX This sequence represents a PCR primer that can be used in the method of  
 CC the invention. The method is for genetic diagnosis using human  
 CC mitochondrial DNA where there is at least one base replacement from among  
 CC the following five replacements: the 3010th base is changed from guanine  
 CC to adenine; the 4883rd base from cytosine to thymine; the 5178th base  
 CC from cytosine to adenine; the 8414th base from cytosine to thymine; and  
 CC the 14668th base from cytosine to thymine. The method can be used for  
 CC diagnosing the probability of contracting adult diseases. A confirmation  
 CC of base replacement can give a diagnosis of the level of probability of  
 CC contraction of adult diseases  
 XX

SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 2; Length 20;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+04;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACTCTTCAGGAGCGG 18

```
Db      20 ATTCTTGCACGAACGG 4
      |||||
RESULT 30
ACC70917/c
ID ACC70917 standard; DNA; 20 BP.
XX
AC ACC70917;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human cytochrome b PCR primer #10.
XX
KW Human; mitochondrial; Parkinson's disease; cytochrome b; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200303737-A1.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-JP010640.
XX
PR 17-OCT-2001; 2001JP-00318805.
XX
PA (GIFU-) GIFU INT INST BIOTECHNOLOGY.
XX
PI Tanaka M;
XX
DR WPI; 2003-393541/37.
XX
PT Gene detection method using human mitochondrial DNA to reveal and confirm
PT amino acid substitution advantageous or disadvantageous in prolonged
PT survival of human, useful for diagnosis of Parkinson's disease.
XX
PS Disclosure; Page 7; 35pp; Japanese.
XX
CC The present invention relates to a detection method using human
CC mitochondrial (mt) DNA. The method comprises detecting the replacement of
CC a base accompanying an amino acid substitution in a protein encoded by
CC its base sequence in a human mitochondrial DNA base sequence. The method
CC is useful for diagnosis of Parkinson's disease, and in health checks and
CC assessing risks for other adult diseases. The present sequence is a PCR
CC primer, which was used to illustrate the invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
      Query Match 61.0%; Score 12.2; DB 8; Length 20;
      Best Local Similarity 82.4%; Pred. No. 4.1e+04;
      Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ACTCTTGACGAAGCGG 18
      |||||
Db 20 ATTCTTGCACGAACGG 4
      |||||
RESULT 31
ADM14320/c
ID ADM14320 standard; DNA; 20 BP.
XX
AC ADM14320;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:507.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
      Query Match 61.0%; Score 12.2; DB 12; Length 20;
      Best Local Similarity 82.4%; Pred. No. 4.1e+04;
      Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TCTTGCAGGACGGCT 20
      |||||
Db 20 TCTTGCAGGACGGCT 4
      |||||
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
XX
SY Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
CC Claim 4; SEQ ID NO 507; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
```

```
RESULT 32
ADM14505/c
ID ADM14505 standard; DNA; 20 BP.
XX
XX
AC ADM14505;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:692.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulatory; cardiatic; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 692; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX CC9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiatic, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
```

```
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g.; inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 61.0%; Score 12.2; DB 12; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TCTTGCAGGAGCGGCT 20
Db 19 TCCTGCACGAAGTGCT 3
RESULT 33
AAF4592/c
ID AAF46592 standard; DNA; 15 BP.
XX
XX AAF46592;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP3 oligonucleotide #12.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional), and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 7; Page 44; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
```

XX SQ Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 60.0%; Score 12; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCAGGAGCGGC 19  
|||||  
DB 12 GCAGGAGCGGC 1

RESULT 34  
AAF4588/C  
ID AAF46588 standard; DNA; 15 BP.  
XX AC AAF46588;  
DT 30-MAR-2001 (first entry)  
XX IGFBP3 oligonucleotide #8.  
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX OS Homo sapiens.  
XX WO200078341-A1.  
XX PD 28-DEC-2000.  
XX PF 21-JUN-2000; 2000WO-AU000693.  
XX PR 21-JUN-1999; 99US-0140345P.  
XX PA (MURD-) MURDOCH CHILDRENS RES INST.  
XX PI Wraight CJ, Werther GA, Edmondson SR;  
XX WPI; 2001-041421/05.  
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX Example 7; Page 44; 201pp; English.  
XX The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX SQ Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 60.0%; Score 12; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CAGGAAGCGGCT 20  
|||||  
DB 15 CAGGAAGCGGCT 4

RESULT 35  
ABT34760/C  
ID ABT34760 standard; DNA; 17 BP.  
XX AC ABT34760;  
DT 12-JUN-2003 (first entry)  
XX Tumour suppression related human fukutin oligo SEQ ID No 397.  
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX OS Homo sapiens.  
XX WO2003025175-A2.  
XX PD 27-MAR-2003.  
XX PF 17-SEP-2002; 2002WO-IB004208.  
XX PR 17-SEP-2001; 2001FR-00011978.  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX Telferman A, Amson R, Tuijnder M;  
XX WPI; 2003-313353/30.  
XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX Disclosure; Page 80; 720pp; French.  
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX SQ Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 60.0%; Score 12; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.1e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 ACTCTTGACGGA 13
      |||||
Db      14 ACTCTTGACGGA 3

RESULT 36
ACC54373
ID      ACC54373 standard; DNA; 17 BP.
XX
AC      ACC54373;
XX
DT      27-JUN-2003 (first entry)
XX
DE      Human tumour suppressor sequence #3140.
XX
KW      ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW      tumour regression; apoptosis; virus resistance; diagnosis;
KW      cellular degeneration.
XX
OS      Homo sapiens.
XX
PN      FR2826373-Al.
XX
PD      27-DEC-2002.
XX
PF      20-JUN-2001; 2001FR-00008139.
XX
PR      20-JUN-2001; 2001FR-00008139.
XX
PA      (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI      Tuijnder M, Telerman A, Amson R;
XX
WPI; 2003-250498/25.
XX
New nucleic acid sequences associated with tumor suppression, regression,
PT      apoptosis or virus resistance are useful to diagnose and treat viral
PT      disease, development of tumor cells and cell degeneration.
XX
Claim 1; Page 765; 798pp; French.
XX
This sequence represents an isolated nucleic acid sequence associated
CC      with tumour suppression or regression, apoptosis or virus resistance. The
CC      invention relates to these sequences or sequences having at least 80%
CC      identity to them, and polypeptides encoded by the sequences or
CC      polypeptides having 80% identity to the polypeptide sequences. The
CC      invention is used to diagnose or treat viral disease or disease
CC      characterized by development of tumour cells or cellular degeneration
XX
SQ      Sequence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

Query Match      60.0%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TCTTCGAGGAG 15
      |||||
Db      3 TCTTCGAGGAG 14

RESULT 37
ADF87984/c
ID      ADF87984 standard; DNA; 19 BP.
XX
AC      ADF87984;
XX
DT      26-FEB-2004 (first entry)
XX
DE      Single nucleotide polymorphism detection primer, SEQ ID NO 1567.
XX
KW      human; single nucleotide polymorphism; microarray; side effect; ss;
KW      primer; PCR.

XX      Synthetic.
OS      Homo sapiens.
XX
PN      JP2003235571-A.
XX
PD      26-AUG-2003.
XX
PF      12-FEB-2002; 2002JP-00034717.
XX
PR      12-FEB-2002; 2002JP-00034717.
XX
PA      (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
WPI; 2003-820454/77.
XX
Novel polynucleotide useful for detecting single nucleotide polymorphisms
PT      in human gene.
XX
Claim 2; SEQ ID NO 1567; 704pp; Japanese.
XX
The invention relates to a novel polynucleotide isolated and purified
CC      from a human gene having any one of 935 fully defined sequences as given
CC      in specification, or a sequence having a base substitution. The invention
CC      further relates to: an oligonucleotide containing single nucleotide
CC      polymorphisms; a PCR primer set chosen from the combination of two DNA
CC      fragments from any one of 1220 fully defined sequences as given in
CC      specification; a labelling probe containing the SNP containing oligo; and
CC      a microarray equipped with the SNP containing oligo. The isolated human
CC      gene of the invention is useful for detecting the single nucleotide
CC      polymorphisms in human gene. The isolated human gene is also useful for
CC      diagnosis of disease and determination of side effect to a medical agent.
CC      The isolated human gene is also effective in detecting single nucleotide
CC      polymorphisms in a human gene. This polynucleotide sequence represents
CC      one of the PCR primers used in the single nucleotide polymorphism
CC      detection method of the invention.
XX
Sequence 19 BP; 1 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match      60.0%; Score 12; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CAGGAAGCGGCT 20
      |||||
Db      17 CAGGAAGCGGCT 6

RESULT 38
AAZ74144/c
ID      AAZ74144 standard; DNA; 20 BP.
XX
AC      AAZ74144;
XX
DT      10-SEP-2001 (first entry)
XX
DE      Human biallelic marker downstream amplification primer SEQ ID NO:8500.
XX
KW      Human genome; biallelic marker; high density disequilibrium map;
KW      genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW      haplotyping; hybridisation; identification; characterisation;
KW      amplification; single nucleotide polymorphism; SNP; PCR primer;
KW      diagnosis; ss.
XX
OS      Homo sapiens.
XX
PN      WO9954500-A2.
XX
PD      28-OCT-1999.
XX
PF      21-APR-1999; 99WO-IB0000822.
XX
PR      21-APR-1998; 98US-0082614P.
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PR 23-NOV-1998; 98US-0109732P.
XX (GBST ) GENSET.
PA Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-011267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX Claim 8; Page 2043; 2745pp; English.
PS AA65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
SQ Query Match 60.0%; Score 12; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 5.2e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GACTCTTCGAGGAGCGGCT 20
DB ||||| ||||| ||||| |||||
20 GACTTTTGACTATGACAGAT 1
RESULT 39
ABAO2533
ID ABAO2533 standard; DNA; 16 BP.
XX AC ABAO2533;
XX 18-JUN-2002 (first entry)
XX DE Lipoprotein lipase precursor SNP-5 reverse PCR primer.
XX Single-nucleotide polymorphism; SNP; diabetes; thalassaemia;
KW sickle-cell anaemia; cystic fibrosis; oncogenic mutation; pathogen;
KW paternity; prenatal testing; forensic investigation; genotyping;
KW 3'-5'-exonuclease; point mutation; lipoprotein lipase precursor; LPL;
KW PCR; primer; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "6-carboxy-x-rhodamine (ROX)"
XX WO200181631-A1.
XX 01-NOV-2001.
XX 24-APR-2001; 2001WO-US013136.
XX 25-APR-2000; 2000US-00558245.
XX (DNAS-) DNA SCI INC.
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XX Xu H, Mathies RA;
XX WPI; 2002-049286/06.
XX Analyzing variant sites in nucleic acid, useful e.g. for detecting
XX disease-associated polymorphisms, comprises extension of labeled primer
XX in presence of polymerase with 3'-5'-exonuclease activity.
XX Example 2; Fig 7C; 82pp; English.
XX The present sequence is that of a labelled PCR primer used to amplify and
XX genotype the partial nucleotide sequence of lipoprotein lipase precursor
XX (LPL) surrounding the single-nucleotide polymorphism (SNP)-5 site given
XX in ABA02531. The specification describes a novel method for analysing a
XX variant site (VS) in a target nucleic acid (NA). NA is amplified sequence
XX specifically by extending two primers (P1, P2) in the presence of a
XX polymerase having 3'-5'-exonuclease activity. P1 is labelled on at least
XX one nucleotide (nt) other than the 3'-terminal nt and it anneals to a
XX region that spans VS in the first strand of NA. P2 is complementary to a
XX region in the complementary second strand of NA. If P1 is complementary
XX to the base occupying VS it will be extended to form a labelled product.
XX If P1 is not complementary the polymerase will digest P1 from its 3'-end,
XX removing the label, and any extension product will be unlabelled. The
XX extension products are analysed for absence/presence of the label. The
XX method of the invention is particularly used to detect point mutations
XX and SNPs, e.g. for diagnosis and prognosis of diabetes, thalassaemia,
XX sickle-cell anaemia, cystic fibrosis or oncogenic mutations, or for
XX assessing predisposition to these conditions or monitoring the effect of
XX treatments. Other applications are detecting pathogens (including those
XX with altered pathogenicity or drug resistance); resolving paternity
XX disputes, and in prenatal testing or forensic investigations. The method
XX can be used for simultaneous analysis of many different VS, in one or
XX more targets, providing very high throughput and rapid genotyping
XX Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
SQ Query Match 59.0%; Score 11.8; DB 6; Length 16;
Best Local Similarity 86.7%; Pred. No. 6.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ACTCTTCGAGGAGC 16
DB ||||| ||||| ||||| |||||
1 ACCCTTCGAGGCAGC 15
RESULT 40
AAFO7158
ID AAFO7158 standard; DNA; 17 BP.
XX AC AAFO7158;
XX 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #3415.
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX Homo sapiens.
XX WO2000061729-A2.
XX 19-OCT-2000.
XX 11-APR-2000; 2000WO-US009721.
XX 12-APR-1999; 99US-0129390P.
XX (RIBO-) RIBOZYME PHARM INC.
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
```

DR WPI; 2000-647423/62.  
XX Enzymatic and antisense nucleic acid inhibition of repressor genes.  
PT useful for producing e.g. granulocyte colony stimulating factor protein,  
PT interferon alpha and erythropoietin.  
XX  
XX  
PS Claim 54; Page 134; 164pp; English.  
XX  
XX The present invention relates to enzymatic and antisense nucleic acid  
CC molecules that act as inhibitors of the expression of repressor genes  
CC encoding the TR2 Orphan receptor, EAR3/COUP-1, the GATA transcription  
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).  
CC Inhibition of the repressors removes prevents inhibition (and  
CC consequently increases expression of) genes involved in the production of  
CC erythropoietin, granulocyte colony stimulating factor protein and  
CC interferon alpha  
XX  
SQ Sequence 17 BP; 6 A; 2 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 59.0%; Score 11.8; DB 3; Length 17;  
Best Local Similarity 86.7%; Pred. No. 6.4e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GACTCTTGCAGGAG 15  
||| |||||  
DB 1 GACTATTTCAGGAG 15

Search completed: August 6, 2005, 15:37:05  
Job time : 236 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 15:33:37 ; Search time 341 Seconds  
(without alignments)

380.195 Million cell updates/sec

Title: US-10-773-678-342

Perfect score: 20

Sequence: 1 gactcttcaggagcggt 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 1713812

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 20    | 100.0       | 20     | 21 | US-10-773-678-342 |
| 2          | 19    | 95.0        | 20     | 21 | US-10-773-678-179 |
| 3          | 19    | 95.0        | 20     | 21 | US-10-773-678-341 |
| 4          | 18    | 90.0        | 20     | 21 | US-10-773-678-343 |
| 5          | 17    | 85.0        | 20     | 21 | US-10-773-678-340 |
| 6          | 17    | 85.0        | 20     | 21 | US-10-773-678-344 |
| 7          | 16    | 80.0        | 20     | 22 | US-10-857-715-201 |

|    |      |      |    |    |                      |                   |
|----|------|------|----|----|----------------------|-------------------|
| 8  | 15   | 75.0 | 20 | 21 | US-10-773-678-339    | Sequence 339, App |
| 9  | 15   | 75.0 | 20 | 21 | US-10-773-678-345    | Sequence 345, App |
| 10 | 14   | 70.0 | 20 | 9  | US-09-758-881-19     | Sequence 19, Appl |
| 11 | 14   | 70.0 | 20 | 21 | US-10-773-678-19     | Sequence 1012, Ap |
| 12 | 13.6 | 68.0 | 20 | 19 | US-10-671-395-1012   | Sequence 1350, Ap |
| 13 | 12.8 | 64.0 | 17 | 17 | US-10-339-674-1350   | Sequence 1351, Ap |
| 14 | 12.8 | 64.0 | 18 | 17 | US-10-339-674-1351   | Sequence 1348, Ap |
| 15 | 12.8 | 64.0 | 19 | 17 | US-10-339-674-1348   | Sequence 1349, Ap |
| 16 | 12.8 | 64.0 | 19 | 17 | US-10-339-674-1349   | Sequence 134, App |
| 17 | 12.8 | 64.0 | 20 | 9  | US-09-752-639-134    | Sequence 134, App |
| 18 | 12.8 | 64.0 | 20 | 9  | US-09-984-198-134    | Sequence 134, App |
| 19 | 12.8 | 64.0 | 20 | 21 | US-10-967-092-134    | Sequence 134, App |
| 20 | 12.8 | 64.0 | 20 | 24 | US-11-011-500-134    | Sequence 571, App |
| 21 | 12.6 | 63.0 | 20 | 19 | US-10-671-395-571    | Sequence 1013, Ap |
| 22 | 12.6 | 63.0 | 20 | 19 | US-10-671-395-1013   | Sequence 1512, Ap |
| 23 | 12.4 | 62.0 | 17 | 22 | US-10-984-919-1512   | Sequence 79, Appl |
| 24 | 12.4 | 62.0 | 20 | 14 | US-10-138-316-79     | Sequence 79, Appl |
| 25 | 12.4 | 62.0 | 20 | 16 | US-10-368-643-79     | Sequence 129, App |
| 26 | 12.4 | 62.0 | 20 | 19 | US-10-714-796-129    | Sequence 161, App |
| 27 | 12.4 | 62.0 | 20 | 19 | US-10-714-796-161    | Sequence 79, Appl |
| 28 | 12.4 | 62.0 | 20 | 20 | US-10-861-520-79     | Sequence 79, Appl |
| 29 | 12.4 | 62.0 | 20 | 21 | US-10-911-678-79     | Sequence 8114, Ap |
| 30 | 12.2 | 61.0 | 17 | 9  | US-09-866-108-8114   | Sequence 544, App |
| 31 | 12.2 | 61.0 | 17 | 10 | US-09-730-2898-544   | Sequence 8114, Ap |
| 32 | 12.2 | 61.0 | 17 | 19 | US-10-723-361-8114   | Sequence 507, App |
| 33 | 12.2 | 61.0 | 20 | 19 | US-10-671-395-507    | Sequence 692, App |
| 34 | 12.2 | 61.0 | 20 | 19 | US-10-671-395-692    | Sequence 383106,  |
| 35 | 12.2 | 61.0 | 20 | 21 | US-10-719-900-383106 | Sequence 271624,  |
| 36 | 12.2 | 61.0 | 20 | 22 | US-10-719-956-271624 | Sequence 8500, Ap |
| 37 | 12   | 60.0 | 20 | 17 | US-10-349-143-8500   | Sequence 91, Appl |
| 38 | 11.8 | 59.0 | 17 | 10 | US-09-780-533A-91    | Sequence 92, Appl |
| 39 | 11.8 | 59.0 | 17 | 10 | US-09-780-533A-92    | Sequence 997, App |
| 40 | 11.8 | 59.0 | 17 | 15 | US-09-780-533A-997   | Sequence 225, App |
| 41 | 11.8 | 59.0 | 17 | 15 | US-10-060-998-225    | Sequence 226, App |
| 42 | 11.8 | 59.0 | 17 | 15 | US-10-060-998-226    | Sequence 227, App |
| 43 | 11.8 | 59.0 | 17 | 22 | US-10-060-998-227    | Sequence 346, App |
| 44 | 11.8 | 59.0 | 19 | 22 | US-10-888-226-346    | Sequence 760, App |
| 45 | 11.8 | 59.0 | 19 | 22 | US-10-888-226-760    | Sequence 70, Appl |
| 46 | 11.8 | 59.0 | 19 | 22 | US-10-923-522-70     | Sequence 333, App |
| 47 | 11.8 | 59.0 | 19 | 22 | US-10-923-522-333    | Sequence 130, App |
| 48 | 11.8 | 59.0 | 20 | 14 | US-10-181-177-130    | Sequence 1183, Ap |
| 49 | 11.8 | 59.0 | 20 | 17 | US-10-339-674-1183   | Sequence 1184, Ap |
| 50 | 11.6 | 58.0 | 20 | 10 | US-09-972-115A-29    | Sequence 28, Appl |
| 51 | 11.6 | 58.0 | 20 | 16 | US-10-167-241-11     | Sequence 11, Appl |
| 52 | 11.6 | 58.0 | 20 | 16 | US-10-168-517-11     | Sequence 8, Appl  |
| 53 | 11.6 | 58.0 | 20 | 16 | US-10-369-378-38     | Sequence 38, Appl |
| 54 | 11.6 | 58.0 | 20 | 16 | US-10-369-378-39     | Sequence 39, Appl |
| 55 | 11.6 | 58.0 | 20 | 16 | US-10-199-937-173    | Sequence 173, App |
| 56 | 11.6 | 58.0 | 20 | 16 | US-10-199-937-174    | Sequence 174, App |
| 57 | 11.6 | 58.0 | 20 | 17 | US-10-181-874-49     | Sequence 49, Appl |
| 58 | 11.6 | 58.0 | 20 | 17 | US-10-380-873B-18    | Sequence 18, Appl |
| 59 | 11.6 | 58.0 | 20 | 17 | US-10-168-853-18     | Sequence 8, Appl  |
| 60 | 11.6 | 58.0 | 20 | 19 | US-10-671-395-340    | Sequence 340, App |
| 61 | 11.6 | 58.0 | 20 | 19 | US-10-698-689-110    | Sequence 110, App |
| 62 | 11.4 | 57.0 | 15 | 21 | US-10-946-498A-12    | Sequence 12, Appl |
| 63 | 11.4 | 57.0 | 15 | 22 | US-10-984-919-1599   | Sequence 1599, Ap |
| 64 | 11.4 | 57.0 | 15 | 22 | US-10-763-367A-13    | Sequence 13, Appl |
| 65 | 11.4 | 57.0 | 16 | 17 | US-10-415-247-8      | Sequence 8, Appl  |
| 66 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-115    | Sequence 115, App |
| 67 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-116    | Sequence 116, App |
| 68 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-117    | Sequence 117, App |
| 69 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-118    | Sequence 118, App |
| 70 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-119    | Sequence 119, App |
| 71 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-6215   | Sequence 6215, Ap |
| 72 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-6216   | Sequence 6216, Ap |
| 73 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-6217   | Sequence 6217, Ap |
| 74 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-6218   | Sequence 6218, Ap |
| 75 | 11.4 | 57.0 | 17 | 9  | US-09-866-108-6219   | Sequence 6219, Ap |
| 76 | 11.4 | 57.0 | 17 | 9  | US-10-060-830-121    | Sequence 121, App |
| 77 | 11.4 | 57.0 | 17 | 14 | US-10-060-830-122    | Sequence 122, App |
| 78 | 11.4 | 57.0 | 17 | 14 | US-10-060-830-123    | Sequence 123, App |
| 79 | 11.4 | 57.0 | 17 | 14 | US-10-060-830-124    | Sequence 124, App |
| 80 | 11.4 | 57.0 | 17 | 14 | US-10-060-830-125    | Sequence 125, App |

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c 81 11.4 57.0 17 14 US-10-060-830-125 Sequence 125, App
82 11.4 57.0 17 19 US-10-723-361-115 Sequence 115, App
83 11.4 57.0 17 19 US-10-723-361-116 Sequence 116, App
84 11.4 57.0 17 19 US-10-723-361-117 Sequence 117, App
85 11.4 57.0 17 19 US-10-723-361-118 Sequence 118, App
86 11.4 57.0 17 19 US-10-723-361-119 Sequence 119, App
87 11.4 57.0 17 19 US-10-723-361-120 Sequence 120, App
88 11.4 57.0 17 19 US-10-723-361-121 Sequence 121, App
89 11.4 57.0 17 19 US-10-723-361-122 Sequence 122, App
90 11.4 57.0 17 19 US-10-723-361-123 Sequence 123, App
91 11.4 57.0 17 19 US-10-723-361-124 Sequence 124, App
92 11.4 57.0 20 10 US-09-906-158-19 Sequence 19, Appl
93 11.4 57.0 20 17 US-10-388-263-468 Sequence 468, App
94 11.4 57.0 20 17 US-10-289-762-6247 Sequence 6247, App
95 11.4 57.0 20 17 US-10-363-198-51 Sequence 51, Appl
96 11.4 57.0 20 19 US-10-316-516-76 Sequence 76, Appl
97 11.4 57.0 20 19 US-10-316-516-129 Sequence 129, App
98 11.4 57.0 20 19 US-10-714-796-168 Sequence 168, App
99 11.4 57.0 20 22 US-10-257-158A-7002 Sequence 7002, App
100 11.4 57.0 20 24 US-11-039-629-253 Sequence 253, App
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## ALIGNMENTS

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RESULT 1
US-10-773-678-342
; Sequence 342, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 342
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-342
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Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GACTCTTGCGAGGAGCGGCT 20
|||||
Db 1 GACTCTTGCGAGGAGCGGCT 20
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RESULT 2
US-10-773-678-179
; Sequence 179, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
```

```
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-179
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Query Match 95.0%; Score 19; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GACTCTTGCGAGGAGCGGC 19
|||||
Db 2 GACTCTTGCGAGGAGCGGC 20
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RESULT 3
US-10-773-678-341
; Sequence 341, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 341
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-341
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Query Match 95.0%; Score 19; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2 ACTCTTGCGAGGAGCGGCT 20
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Db 1 ACTCTTGCGAGGAGCGGCT 19
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RESULT 4
US-10-773-678-343
; Sequence 343, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
```

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; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 343
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-343

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Query Match          90.0%; Score 18; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GACTCTTGCAGGAGCGG 18
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Db 3 GACTCTTGCAGGAGCGG 20

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RESULT 5
US-10-773-678-340
; Sequence 340, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-340

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Query Match          85.0%; Score 17; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 4 TCTTGCAAGGCGCT 20
    |||||
Db 1 TCTTGCAAGGCGCT 17

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RESULT 6
US-10-773-678-344
; Sequence 344, Application US/10773678
; Publication No. US20050074879A1

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; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 344
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-344

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Query Match          85.0%; Score 17; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GACTCTTGCAGGAGCG 17
    |||||
Db 4 GACTCTTGCAGGAGCG 20

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RESULT 7
US-10-857-715-201
; Sequence 201, Application US/10857715
; Publication No. US20050164218A1
; GENERAL INFORMATION:
; APPLICANT: Agus David
; APPLICANT: Baker Joffre
; APPLICANT: Natale Ron
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Gene Expression Markers for Response to
; TITLE OF INVENTION: EGFR Inhibitors Drugs
; FILE REFERENCE: 39740/0011
; CURRENT APPLICATION NUMBER: US/10/857,715
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474,908
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: reverse primer
US-10-857-715-201

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Query Match          80.0%; Score 16; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 CTTGCAGGAGCGCT 20
    |||||
Db 1 CTTGCAGGAGCGCT 16

```

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RESULT 8
US-10-773-678-339
; Sequence 339, Application US/10773678
; Publication No. US20050074879A1

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US-10-773-678-345

GENERAL INFORMATION:  
; APPLICANT: Karras, James G  
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3  
; FILE REFERENCE: ISPH-0828  
; CURRENT APPLICATION NUMBER: US/10/773,678  
; CURRENT FILING DATE: 2004-02-06  
; PRIOR FILING DATE: 10/713,139  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 09/758,881  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09054  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 09/288,461  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 402  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 339  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense oligonucleotide

US-10-773-678-339

Query Match 75.0%; Score 15; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20  
| | | | | | | | | |  
Db 1 TTGCAGGAAGCGGCT 15

RESULT 9

US-10-773-678-345

Sequence 345, Application US/10773678  
Publication No. US20050074879A1  
GENERAL INFORMATION:  
; APPLICANT: Karras, James G  
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3  
; FILE REFERENCE: ISPH-0828  
; CURRENT APPLICATION NUMBER: US/10/773,678  
; CURRENT FILING DATE: 2004-02-06  
; PRIOR FILING DATE: 10/713,139  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 09/758,881  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09054  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 09/288,461  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 402  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 345  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense oligonucleotide

US-10-773-678-345

Query Match 75.0%; Score 15; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAAG 15  
| | | | | | | | | |  
Db 6 GACTCTTGCAAG 20

RESULT 10

US-09-758-881-19

Sequence 19, Application US/09758881  
Patent No. US20010029250A1  
GENERAL INFORMATION:  
; APPLICANT: Karras, James G  
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3  
; FILE REFERENCE: ISPH-0532  
; CURRENT APPLICATION NUMBER: US/09/758,881  
; CURRENT FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09054  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 09/288,461  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-758-881-19

Query Match 70.0%; Score 14; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAAGAA 14  
| | | | | | | | | |  
Db 7 GACTCTTGCAAGAA 20

RESULT 11

US-10-773-678-19

Sequence 19, Application US/10773678  
Publication No. US20050074879A1  
GENERAL INFORMATION:  
; APPLICANT: Karras, James G  
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3  
; FILE REFERENCE: ISPH-0828  
; CURRENT APPLICATION NUMBER: US/10/773,678  
; CURRENT FILING DATE: 2004-02-06  
; PRIOR FILING DATE: 10/713,139  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 09/758,881  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09054  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 09/288,461  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 402  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-773-678-19

Query Match 70.0%; Score 14; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAAGAA 14  
| | | | | | | | | |  
Db 7 GACTCTTGCAAGAA 20

RESULT 12

US-10-671-395-1012/c

```
; Sequence 1012, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1012
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1012

Query Match      68.0%; Score 13.6; DB 19; Length 20;
Best Local Similarity 80.0%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCGACGAAGCGGCT 20
   ||||| ||||| ||||| |||||
DB 20 GATTCTCTGCACGAAGTGCT 1

RESULT 13
US-10-339-674-1350/c
; Sequence 1350, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1350
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1734068)...(1734084)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1777
US-10-339-674-1350

Query Match      64.0%; Score 12.8; DB 17; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGCGGC 19
   ||||| ||||| ||||| |||||
DB 17 TCTTGCAGGATCGGC 2

RESULT 14
US-10-339-674-1351
; Sequence 1351, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
US-10-339-674-1351
```

```
; SEQ ID NO 1351
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1734068)...(1734085)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1778
US-10-339-674-1351

Query Match      64.0%; Score 12.8; DB 17; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGCGGC 19
   ||||| ||||| ||||| |||||
DB 2 TCTTGCAGGATCGGC 17

RESULT 15
US-10-339-674-1348/c
; Sequence 1348, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1348
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1734067)...(1734085)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 177
US-10-339-674-1348

Query Match      64.0%; Score 12.8; DB 17; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGCGGC 19
   ||||| ||||| ||||| |||||
DB 18 TCTTGCAGGATCGGC 3

RESULT 16
US-10-339-674-1349
; Sequence 1349, Application US/10339674
; Publication No. US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1349
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (1734067)...(1734085)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 177
US-10-339-674-1349

Query Match      64.0%; Score 12.8; DB 17; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGCGGC 19
   ||||| ||||| ||||| |||||
DB 18 TCTTGCAGGATCGGC 3
```

QY 4 TCTTGCAGGAGCGGC 19  
|||||  
Db 2 TCTTCCGAGTCTGC 17

## RESULT 17

US-09-752-639-134  
; Sequence 134, Application US/09752639  
; Patent No. US20020091243A1  
; GENERAL INFORMATION:  
; APPLICANT: Gatanaga, T.  
; APPLICANT: Granger, G.A.  
; TITLE OF INVENTION: Factors Altering Tumor Necrosis  
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods  
; TITLE OF INVENTION: of Use Thereof  
; NUMBER OF SEQUENCES: 154  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/752,639  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US99/10793  
; FILING DATE:  
; APPLICATION NUMBER: 09/081,385  
; FILING DATE:  
; APPLICATION NUMBER: 08/964,747  
; FILING DATE: 05-NOV-1997  
; APPLICATION NUMBER: 60/030,761  
; FILING DATE: 06-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wu, Frank  
; REGISTRATION NUMBER: 41,386  
; REFERENCE/DOCKET NUMBER: 22000-20577.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 134:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-752-639-134  
Query Match 64.0%; Score 12.8; DB 9; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 TCTTGCAGGAGCGGC 19  
|||||  
Db 1 TCTTCCGAGTCTGC 16

RESULT 18

US-09-984-198-134  
; Sequence 134, Application US/09984198  
; Patent No. US20020106679A1  
; GENERAL INFORMATION:  
; APPLICANT: Gatanaga, T.  
; APPLICANT: Granger, G.A.

; TITLE OF INVENTION: Factors Altering Tumor Necrosis  
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods  
; TITLE OF INVENTION: of Use Thereof  
; NUMBER OF SEQUENCES: 154  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/984,198  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US99/10793  
; FILING DATE:  
; APPLICATION NUMBER: 09/081,385  
; FILING DATE:  
; APPLICATION NUMBER: 08/964,747  
; FILING DATE: 05-NOV-1997  
; APPLICATION NUMBER: 60/030,761  
; FILING DATE: 06-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wu, Frank  
; REGISTRATION NUMBER: 41,386  
; REFERENCE/DOCKET NUMBER: 22000-20577.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 134:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-984-198-134  
Query Match 64.0%; Score 12.8; DB 9; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 TCTTGCAGGAGCGGC 19  
|||||  
Db 1 TCTTCCGAGTCTGC 16

RESULT 19

US-10-967-092-134  
; Sequence 134, Application US/10967092  
; Publication No. US20050090647A1  
; GENERAL INFORMATION:  
; APPLICANT: Gatanaga, T.  
; APPLICANT: Granger, G.A.  
; TITLE OF INVENTION: Factors Altering Tumor Necrosis  
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods  
; TITLE OF INVENTION: of Use Thereof  
; NUMBER OF SEQUENCES: 154  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA: US/10/967,092  
FILING DATE: 15-Oct-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/712,813  
FILING DATE: 13-Nov-2000  
APPLICATION NUMBER: US/09/081,385  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/964,747  
FILING DATE: 05-Nov-1997  
APPLICATION NUMBER: 60/030,761  
FILING DATE: 06-Nov-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Wu, Frank  
REGISTRATION NUMBER: 41,386  
REFERENCE/DOCKET NUMBER: 22000-20577.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 134:  
US-10-967-092-134

Query Match 64.0%; Score 12.8; DB 21; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTTCAGGAGCGGC 19  
||| ||||| |||  
Db 1 TCTTCAGGAGCTGC 16

RESULT 20  
US-11-011-500-134  
; Sequence 134, Application US/11011500  
; Publication No. US20050158826A1  
; GENERAL INFORMATION:  
; APPLICANT: Gatanaga, T.  
; TITLE OF INVENTION: Factors Altering Tumor Necrosis  
; Factor Receptor Releasing Enzyme Activity, and Methods  
; of Use Thereof  
NUMBER OF SEQUENCES: 154  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/011,500  
FILING DATE: 13-Dec-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/10/967,092  
FILING DATE: 15-Oct-2004

APPLICATION NUMBER: US/09/712,813  
FILING DATE: 13-Nov-2000  
APPLICATION NUMBER: US/09/081,385  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/964,747  
FILING DATE: 05-Nov-1997  
APPLICATION NUMBER: 60/030,761  
FILING DATE: 06-Nov-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Wu, Frank  
REGISTRATION NUMBER: 41,386  
REFERENCE/DOCKET NUMBER: 22000-20577.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 134:  
US-11-011-500-134

Query Match 64.0%; Score 12.8; DB 24; Length 20;  
Best Local Similarity 87.5%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTTCAGGAGCGGC 19  
||| ||||| |||  
Db 1 TCTTCAGGAGCTGC 16

RESULT 21  
US-10-671-395-571/c  
; Sequence 571, Application US/10671395  
; Publication No. US20040132063A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Gierse, James K.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE  
; FILE OF INVENTION: EXPRESSION  
; FILE REFERENCE: 1179/1/US  
; CURRENT APPLICATION NUMBER: US/10/671,395  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: 60/413,549  
; PRIOR FILING DATE: 2002-09-25  
; NUMBER OF SEQ ID NOS: 1809  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 571  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Human PGE2 antisense  
US-10-671-395-571

Query Match 63.0%; Score 12.6; DB 19; Length 20;  
Best Local Similarity 78.9%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAGCGGC 19  
||| ||||| |||  
Db 19 GATTCTGCAGGAGTGGC 1

RESULT 22  
US-10-671-395-1013/c  
; Sequence 1013, Application US/10671395  
; Publication No. US20040132063A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.

; APPLICANT: Gierse, James K  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE  
; FILE REFERENCE: 1179/1/US  
; CURRENT APPLICATION NUMBER: US/10/671,395  
; PRIOR FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: 60/413,549  
; PRIOR FILING DATE: 2002-09-25  
; NUMBER OF SEQ ID NOS: 1809  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1013  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Human PGE2 antisense  
US-10-671-395-1013

Query Match 63.0%; Score 12.6; DB 19; Length 20;  
Best Local Similarity 78.9%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGAGGCGCT 20  
| | | | | | | | | | | | | | | | | | | |  
Db 20 ATTCTGACGAGTGGCT 2

RESULT 23  
US-10-984-919-1512  
; Sequence 1512, Application US/10984919  
; Publication No. US20050130927A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiefen, Karl-Hermann  
; APPLICANT: Brysch, Wolfgang  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
; FILE REFERENCE: 10496/P63763USO  
; CURRENT APPLICATION NUMBER: US/10/984,919  
; PRIOR FILING DATE: 2004-11-10  
; PRIOR APPLICATION NUMBER: US/09/341,700  
; PRIOR FILING DATE: 1999-09-24  
; PRIOR APPLICATION NUMBER: PCT/EP98/00497  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: EP 97 101 531.8  
; PRIOR FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 1764  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1512  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
US-10-984-919-1512

Query Match 62.0%; Score 12.4; DB 22; Length 17;  
Best Local Similarity 92.9%; Pred. No. 1.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGAGG 15  
| | | | | | | | | | | | | | | |  
Db 4 ACTCTTGACGGTAG 17

RESULT 24  
US-10-138-316-79/c  
; Sequence 79, Application US/10138316  
; Publication No. US20030054380A1  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH

; TITLE OF INVENTION: CAUSE ARHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING  
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE  
; FILE REFERENCE: 2323-162  
; CURRENT APPLICATION NUMBER: US/10/138,316  
; PRIOR FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 09/444,295  
; PRIOR FILING DATE: 1999-11-22  
; PRIOR APPLICATION NUMBER: 09/135,020  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 08/921,068  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; PRIOR APPLICATION NUMBER: 60/094,477  
; PRIOR FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 79  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-138-316-79

Query Match 62.0%; Score 12.4; DB 14; Length 20;  
Best Local Similarity 92.9%; Pred. No. 1.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAGCGGCT 20  
| | | | | | | | | | | | | | | |  
Db 18 TGCAGGAGCGGAT 5

RESULT 25  
US-10-368-643-79/c  
; Sequence 79, Application US/10368643  
; Publication No. US20030170708A1  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Curran, Mark E.  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Connors, Timothy D.  
; APPLICANT: Burn, Timothy C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE  
; FILE REFERENCE: 2323-163  
; CURRENT APPLICATION NUMBER: US/10/368,643  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 09/597,731  
; PRIOR FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: US 09/135,010  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: US 60/094,477  
; PRIOR FILING DATE: 1998-07-29  
; PRIOR APPLICATION NUMBER: US 08/921,068  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: US 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: US 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 79  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-368-643-79

Query Match 62.0%; Score 12.4; DB 16; Length 20;  
Best Local Similarity 92.9%; Pred. No. 1.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 7 TGCAGGAAGCGCT 20
Db 18 TGCAGGAAGCGGAT 5

RESULT 26
US-10-714-796-129/c
; Sequence 129, Application US/10714796
; Publication No. US20040180847A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
; FILE REFERENCE: ISHT-1004
; CURRENT APPLICATION NUMBER: US/10/714,796
; PRIOR FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 10/156,603
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-714-796-129

Query Match 62.0%; Score 12.4; DB 19; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTTCAGGAAGCG 17
Db 20 TCTTCAGGAAGTG 7

RESULT 27
US-10-714-796-161/c
; Sequence 161, Application US/10714796
; Publication No. US20040180847A1
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
; FILE REFERENCE: ISHT-1004
; CURRENT APPLICATION NUMBER: US/10/714,796
; PRIOR FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 10/156,603
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-714-796-161

Query Match 62.0%; Score 12.4; DB 19; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTTCAGGAAGCG 17
Db 19 TCTTCAGGAAGTG 6

RESULT 28
US-10-861-520-79/c
; Sequence 79, Application US/10861520
; Publication No. US20040235038A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
```

```
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-167
; CURRENT APPLICATION NUMBER: US/10/861,520
; CURRENT FILING DATE: 2004-06-07
; PRIOR APPLICATION NUMBER: 10/138,316
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-861-520-79

Query Match 62.0%; Score 12.4; DB 20; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGCT 20
Db 18 TGCAGGAAGCGGAT 5

RESULT 29
US-10-911-678-79/c
; Sequence 79, Application US/10911678
; Publication No. US20050003439A1
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; APPLICANT: Sanguinetti, Michael C.
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-169
; CURRENT APPLICATION NUMBER: US/10/911,678
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: 10/138,316
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-911-678-79
```

Query Match 62.0%; Score 12.4; DB 21; Length 20;  
Best Local Similarity 92.9%; Pred. No. 1.9e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20  
|||||

Db 18 TGCAGGAAGCGGAT 5

## RESULT 30

US-09-866-108-8114  
; Sequence 8114, Application US/09866108  
; Patent No. US2002004800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: A601CA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: A601CA Sequence Listing Engine  
; SEQ ID NO 8114  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-8114

Query Match 61.0%; Score 12.2; DB 9; Length 17;  
Best Local Similarity 82.4%; Pred. No. 2.4e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTCGAGGAGCGGCT 20  
|||||

Db 1 TCTTCGAGGAGCGGCT 17

## RESULT 31

US-09-730-289B-544/c  
; Sequence 544, Application US/09730289B  
; Publication No. US20030050259A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
; FILE REFERENCE: MBH00-864-A (400/006)  
; CURRENT APPLICATION NUMBER: US/09/730,289B  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/169,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 3897  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 544  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-730-289B-544

Query Match 61.0%; Score 12.2; DB 10; Length 17;  
Best Local Similarity 82.4%; Pred. No. 2.4e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCGAGGAGCGG 18  
|||||

Db 17 ACTCTTCGAGGAGTGG 1

## RESULT 32

US-10-723-361-8114  
; Sequence 8114, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: A601CA Sequence Listing Engine  
; SEQ ID NO 8114  
; LENGTH: 17  
; TYPE: DNA

[illegible]; TITLE OF INVENTION: STAT  
; FILE REFERENCE: GENSET.0200

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; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8500
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-15968 for SEQ 635, in compleme
US-10-349-143-8500

Query Match 60.0%; Score 12; DB 17; Length 20;
Best Local Similarity 75.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGGCT 20
Db 20 GACTTTTGCCTAAGCAGAT 1

RESULT 38
US-09-780-533A-91/c
; Sequence 91, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-91

Query Match 59.0%; Score 11.8; DB 10; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
Db 16 TTGAAGAAGCGGCT 2

RESULT 39
US-09-780-533A-92/c
; Sequence 92, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
```

```
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-92
```

```
Query Match 59.0%; Score 11.8; DB 10; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
Db 15 TTGAAGAAGCGGCT 1
```

```
RESULT 40
US-09-780-533A-997/c
; Sequence 997, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 997
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-997
```

```
Query Match 59.0%; Score 11.8; DB 10; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
Db 17 TTGAAGAAGCGGCT 3
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Search completed: August 6, 2005, 16:35:48  
Job time : 342 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 13:40:42 ; Search time 1623 Seconds  
(without alignments)  
469.061 Million cell updates/sec

Title: US-10-773-678-342

Perfect score: 20

Sequence: 1 gactcttcgaggaagcgct 20

Scoring table: IDENTIFY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 12452

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

EST:\*  
1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_hcc:\*  
4: gb\_esc3:\*  
5: gb\_esc4:\*  
6: gb\_esc5:\*  
7: gb\_esc6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 10.6  | 53.0        | 20     | 8     | AZ314365    |
| 2          | 10.4  | 52.0        | 18     | 1     | AJ650912    |
| 3          | 10.2  | 51.0        | 19     | 6     | CD532073    |
| 4          | 10.2  | 51.0        | 20     | 8     | AZ637794    |
| 5          | 9.6   | 48.0        | 20     | 8     | AZ336487    |
| 6          | 9.4   | 47.0        | 19     | 8     | AZ410317    |
| 7          | 9.4   | 47.0        | 19     | 8     | AZ816318    |
| 8          | 9.4   | 47.0        | 20     | 8     | AZ798282    |
| 9          | 9.4   | 45.0        | 19     | 8     | AZ482658    |
| 10         | 9.4   | 45.0        | 19     | 8     | CL661094    |
| 11         | 9.4   | 45.0        | 20     | 5     | BX559186    |
| 12         | 8.8   | 44.0        | 16     | 5     | BQ587767    |
| 13         | 8.8   | 44.0        | 19     | 8     | AZ481008    |
| 14         | 8.8   | 44.0        | 19     | 8     | AZ959942    |
| 15         | 8.6   | 43.0        | 20     | 9     | AJ599745    |
| 16         | 8.4   | 42.0        | 16     | 9     | AJ587896    |
| 17         | 8.4   | 42.0        | 19     | 8     | AZ397615    |
| 18         | 8.4   | 42.0        | 19     | 8     | AZ413661    |
| 19         | 8.4   | 42.0        | 19     | 8     | AZ759607    |
| 20         | 8.4   | 42.0        | 20     | 8     | AZ597307    |
| 21         | 8.4   | 42.0        | 20     | 8     | AZ827842    |
| 22         | 8.4   | 42.0        | 20     | 9     | AG189193    |
| 23         | 8.2   | 41.0        | 13     | 5     | BQ789829    |
| 24         | 8.2   | 41.0        | 18     | 1     | AI042533    |

|    |     |      |    |   |           |
|----|-----|------|----|---|-----------|
| 25 | 8.2 | 41.0 | 18 | 6 | C00629    |
| 26 | 8.2 | 41.0 | 19 | 9 | CL661466  |
| 27 | 8.2 | 41.0 | 18 | 1 | AJ666428  |
| 28 | 8.2 | 41.0 | 19 | 5 | BQ587387  |
| 29 | 8.2 | 41.0 | 19 | 8 | AZ63824   |
| 30 | 8.2 | 41.0 | 19 | 8 | AZ422762  |
| 31 | 8.2 | 41.0 | 19 | 8 | AZ509071  |
| 32 | 8.2 | 41.0 | 19 | 8 | AZ626779  |
| 33 | 8.2 | 41.0 | 20 | 8 | AZ410583  |
| 34 | 8.2 | 41.0 | 20 | 9 | TA2078030 |
| 35 | 8.2 | 41.0 | 19 | 1 | AA916934  |
| 36 | 8.2 | 41.0 | 19 | 3 | CNS09MAX  |
| 37 | 8.2 | 41.0 | 19 | 8 | AZ500630  |
| 38 | 8.2 | 41.0 | 20 | 7 | CF305590  |
| 39 | 8.2 | 41.0 | 20 | 8 | AZ366451  |
| 40 | 8.2 | 41.0 | 20 | 8 | AZ436762  |
| 41 | 8.2 | 41.0 | 20 | 8 | AZ491509  |
| 42 | 8.2 | 41.0 | 20 | 8 | AZ625776  |
| 43 | 8.2 | 41.0 | 20 | 8 | AZ638950  |
| 44 | 8.2 | 41.0 | 20 | 8 | AZ61324   |
| 45 | 8.2 | 41.0 | 15 | 1 | AJ665863  |
| 46 | 8.2 | 41.0 | 17 | 6 | CD531254  |
| 47 | 8.2 | 41.0 | 17 | 6 | CD533040  |
| 48 | 8.2 | 41.0 | 17 | 6 | CF305567  |
| 49 | 8.2 | 41.0 | 17 | 7 | CF305567  |
| 50 | 8.2 | 41.0 | 18 | 9 | AJ590049  |
| 51 | 8.2 | 41.0 | 19 | 1 | AJ660794  |
| 52 | 8.2 | 41.0 | 19 | 7 | CF318426  |
| 53 | 8.2 | 41.0 | 19 | 8 | AZ810098  |
| 54 | 8.2 | 41.0 | 19 | 8 | AZ824929  |
| 55 | 8.2 | 41.0 | 19 | 8 | AZ847888  |
| 56 | 8.2 | 41.0 | 19 | 8 | AZ959942  |
| 57 | 8.2 | 41.0 | 20 | 1 | AI039677  |
| 58 | 8.2 | 41.0 | 20 | 1 | AL045408  |
| 59 | 8.2 | 41.0 | 20 | 1 | AQ074235  |
| 60 | 8.2 | 41.0 | 20 | 8 | AZ482160  |
| 61 | 8.2 | 41.0 | 20 | 8 | AZ483003  |
| 62 | 8.2 | 41.0 | 20 | 8 | AZ665334  |
| 63 | 8.2 | 41.0 | 20 | 8 | AZ779169  |
| 64 | 8.2 | 41.0 | 20 | 8 | AZ787369  |
| 65 | 8.2 | 41.0 | 20 | 8 | AZ946089  |
| 66 | 8.2 | 41.0 | 20 | 8 | AZ961140  |
| 67 | 8.2 | 41.0 | 20 | 9 | AG203570  |
| 68 | 8.2 | 41.0 | 14 | 9 | CL659921  |
| 69 | 8.2 | 41.0 | 17 | 4 | BM395339  |
| 70 | 8.2 | 41.0 | 19 | 1 | AI138366  |
| 71 | 8.2 | 41.0 | 19 | 1 | AJ657561  |
| 72 | 8.2 | 41.0 | 19 | 8 | AZ377971  |
| 73 | 8.2 | 41.0 | 19 | 8 | AZ798955  |
| 74 | 8.2 | 41.0 | 20 | 8 | CL436591  |
| 75 | 8.2 | 41.0 | 20 | 8 | AZ308311  |
| 76 | 8.2 | 41.0 | 20 | 8 | AZ611227  |
| 77 | 8.2 | 41.0 | 20 | 8 | AZ775705  |
| 78 | 8.2 | 41.0 | 20 | 8 | AZ828387  |
| 79 | 8.2 | 41.0 | 11 | 9 | AJ660625  |
| 80 | 8.2 | 41.0 | 12 | 1 | AJ648301  |
| 81 | 8.2 | 41.0 | 15 | 6 | CA851770  |
| 82 | 8.2 | 41.0 | 16 | 1 | AA881100  |
| 83 | 8.2 | 41.0 | 16 | 7 | CF920788  |
| 84 | 8.2 | 41.0 | 16 | 7 | AJ595245  |
| 85 | 8.2 | 41.0 | 17 | 2 | AM247673  |
| 86 | 8.2 | 41.0 | 17 | 4 | BQ927979  |
| 87 | 8.2 | 41.0 | 17 | 5 | BQ519855  |
| 88 | 8.2 | 41.0 | 17 | 9 | AJ589127  |
| 89 | 8.2 | 41.0 | 18 | 5 | BQ586080  |
| 90 | 8.2 | 41.0 | 18 | 6 | CA853355  |
| 91 | 8.2 | 41.0 | 19 | 1 | AI663799  |
| 92 | 8.2 | 41.0 | 19 | 3 | CNS08V62  |
| 93 | 8.2 | 41.0 | 19 | 7 | CK576562  |
| 94 | 8.2 | 41.0 | 19 | 8 | AZ314110  |
| 95 | 8.2 | 41.0 | 19 | 8 | AZ794653  |
| 96 | 8.2 | 41.0 | 19 | 8 | AZ804026  |
| 97 | 8.2 | 41.0 | 19 | 8 | AZ828745  |

|           |            |
|-----------|------------|
| C00629    | HUNG000817 |
| CL661466  | PR10139d   |
| AJ666428  | AJ666428   |
| BQ587387  | S014305-0  |
| AZ63824   | IM0109P06  |
| AZ422762  | IM0201P12  |
| AZ509071  | IM0351A21  |
| AZ626779  | IM0467A14  |
| AZ410583  | IM0182E24  |
| TA2078030 | T. brucei  |
| AA916934  | cn114809.8 |
| CNS09MAX  | Single re  |
| AZ500630  | IM0339A10  |
| AZ814554  | 2M0082P13  |
| CF305590  | HDAL--01-  |
| AZ366451  | IM0115N07  |
| AZ436762  | IM0224G12  |
| AZ491509  | IM0325B09  |
| AZ625776  | IM0465C08  |
| AZ638950  | IM0499E08  |
| AZ61324   | 2M0167A13  |
| AJ665863  | AJ665863   |
| CD531254  | 10B19 Ara  |
| CD533040  | 23N7 Arab  |
| CF305567  | HDAL--01-  |
| AJ590049  | Arcabidops |
| AJ660794  | AJ660794   |
| CF318426  | HD--08-12  |
| AZ810098  | 2M0074N21  |
| AZ824929  | 2M0099P16  |
| AZ847888  | 2M0148G07  |
| AZ959942  | 2M0227L13  |
| AI039677  | DKE20434H  |
| AL045408  | DKE20434E  |
| AQ074235  | 21 PUC8 P  |
| AZ482160  | IM0307G09  |
| AZ483003  | IM0308G19  |
| AZ665334  | IM0546A14  |
| AZ779169  | 2M0015N08  |
| AZ787369  | 2M0033C19  |
| AZ946089  | 2M0207A13  |
| AZ961140  | 2M0229P20  |
| AG203570  | Par. trogl |
| CL659921  | PR10135C   |
| BM395339  | 50072-2-5  |
| AI138366  | q053b01.x  |
| AJ657561  | AJ657561   |
| AZ377971  | IM0132I03  |
| AZ798955  | 2M0056K01  |
| CL436591  | PST3313-N  |
| AZ308311  | IM0011J12  |
| AZ611227  | IM0436E13  |
| AZ775705  | 2M0008P11  |
| AZ828387  | 2M0105P13  |
| AJ660625  | Arcabidops |
| AJ648301  | AJ648301   |
| CA851770  | D16F12 L2  |
| AA881100  | v206d08.r  |
| CF920788  | gmfrhw3-   |
| AJ595245  | Arcabidops |
| AM247673  | 2820207.5  |
| BQ927979  | HNC45-1-G  |
| BQ519855  | IM02580-0  |
| AJ589127  | Arcabidops |
| BQ586080  | B012394-0  |
| CA853355  | B07C12.se  |
| AI663799  | u106a10.x  |
| CNS08V62  | Single re  |
| CK576562  | ICR WTS.1  |
| AZ314110  | IM0030E16  |
| AZ794653  | 2M0048G05  |
| AZ804026  | 2M0064007  |
| AZ828745  | 2M0105J19  |

c 98 7.4 37.0 20 2 AM246466 2821777.3  
99 7.4 37.0 20 7 CF339443  
100 7.4 37.0 20 7 CF921355 CF921355 gmrRw3-

## ALIGNMENTS

## RESULT 1

AZ314365/c

LOCUS 20 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0031507F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0031507 F, genomic survey sequence.

ACCESSION AZ314365  
VERSION AZ314365.1 GI:10360181

KEYWORDS

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Petersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

CONTACT: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0031 row: G column: 07  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

## FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0031507"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptor complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match

53.0%; Score 10.6; DB 8; Length 20;

Best Local Similarity 76.5%; Pred. No. 1.6e+06;  
Matches 13; Conservative 0; Mismatches 4; Indels 0;  
Gaps 0;  
Qy 4 TCTTGACGAGACGGCT 20  
|||||  
Db 20 TCTTCAGGAGACGAGT 4

## RESULT 2

AJ650912/c

LOCUS 18 bp mRNA linear EST 07-JUL-2004  
DEFINITION AJ650912 CSEQRAN19 Sus scrofa cDNA clone C0003276\_L01, mRNA  
sequence.

ACCESSION AJ650912  
VERSION AJ650912.1 GI:49327757

KEYWORDS

SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 18)  
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.  
Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
unpublished (2004)

## JOURNAL

CONTACT: Anderson SI

Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross-match with the -mncore 20  
and -mismatch 12 options. Vector: pBluescript11(KS) R. Site1: EcoRI  
R. Site2: NotI 5' Seg Primer M13p Normalised library constructed  
from pooled ovaries. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.atk-genomics.org.  
Location/Qualifiers

## FEATURES

source

1..18  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0003276\_L01"  
/tissue\_type="ovary"  
/clone\_lib="CSEQRAN19"  
/note="Vector: pBluescript11(KS+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing; Normalised library  
constructed from pooled ovaries"

## ORIGIN

Query Match 52.0%; Score 10.4; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 2e+06;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GCAGGACGGC 19  
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Db 12 GCAGGACGGC 1

RESULT 3  
CD532073 19 bp mRNA linear EST 31-DEC-2003  
LOCUS CD532073/c  
DEFINITION 13104 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA  
3', mRNA sequence.

ACCESSION CD532073  
VERSION CD532073.1 GI:40452085

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 19)  
AUTHORS Guo, Y., Cai, Z. and Gan, S.  
Arabidopsis thaliana (thale cress)  
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

TITLE Transcription of Arabidopsis leaf senescence  
JOURNAL Plant Cell Environ. 27 (5), 521-549 (2004)  
COMMENT Contact: Sheng Gan  
Department of Horticulture  
Cornell University  
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA  
Tel: 607 255 5418  
Fax: 607 255 0599  
Email: sg288@cornell.edu  
Insert Length: 19 Std Error: 0.00  
Seq primer: T7  
POLYA-No.

FEATURES  
source location/Qualifiers

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/lab\_host="E. coli"  
/clone\_lib="Arabidopsis leaf senescence library"  
/note="Organ: Rosette leaf; Vector: pBluescript SKII+;  
Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5  
and #6 (counted from the bottom) were harvested and  
immediately frozen in liquid N2. The leaves were visibly  
yellow excepted for the leaf base areas that were still  
greenish."

## ORIGIN

Query Match 51.0%; Score 10.2; DB 6; Length 19;  
Best Local Similarity 80.0%; Pred. No. 2.6e+06;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTTGACGAGCGGC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 CCGAGGAGGAGCAGC 5

RESULT 4  
AZ637794/c 20 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0497D20F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0497D20 F, genomic survey sequence.  
ACCESSION AZ637794  
VERSION AZ637794.1 GI:1175984  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

TITLE

JOURNAL  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0497 row: D column: 20  
Seq primer: CCGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGM0497D20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/note="Vector: PMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (GI:4732114|9b|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 51.0%; Score 10.2; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2.6e+06;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACTCTTGACGAGAG 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 16 GGCTCTTGAGAGAG 2

RESULT 5  
AZ336487/c 20 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0066J13R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0066J13 R, genomic survey sequence.  
ACCESSION AZ336487  
VERSION AZ336487.1 GI:10405834  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

TITLE

JOURNAL  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0066 row: J column: 13  
Seq primer: CACACAGAAACAGCTATGACG  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES

source

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M006u13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb Plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

## ORIGIN

|                       |                 |                    |           |            |
|-----------------------|-----------------|--------------------|-----------|------------|
| Query Match           | 48.0%;          | Score 9.6;         | DB 8;     | Length 20; |
| Best Local Similarity | 75.0%;          | Pred. No. 5.1e+06; |           |            |
| Matches 12;           | Conservative 0; | Mismatches 4;      | Indels 0; | Gaps 0;    |

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QY      2 ACTCTTCAGGAGCC 17
          ||| ||||| |
Db      17 ACTGTTGCAGGCTGG 2

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| RESULT 6   | LOCUS                    | DEFINITION       |
|------------|--------------------------|------------------|
| AZ410317/c | AZ410317                 | 19 bp DNA linear |
|            | 1M0182L02 Mouse          | GSS 03-OCT-2000  |
|            | clone UUGC1M0182L02 R,   | genomic          |
|            | genomic survey sequence. |                  |

|           |             |
|-----------|-------------|
| ACCESSION | AZ410317    |
| VERSION   | AZ410317.1  |
|           | GI:10534330 |

**SOURCE** Mus musculus (house mouse)

## ORGANISM

REFERENCE  
AUTHORS

| TITLE       | Mouse whole genome scaffolding with paired end reads from 10kb            |
|-------------|---|
| FILE        | mouse_scaffolding_10kb  |
| DESCRIPTION | Mouse whole genome scaffolding with paired end reads from 10kb            |
| DATE        | 2010-01-01  |
| VERSION     | 1.0   |
| AUTHOR      | John Doe  |
| CONTACT     | john.doe@university.edu   |
| PROJECT     | Mouse whole genome scaffolding  |
| STATUS      | Completed   |
| REMARKS     | Initial scaffolding results show high coverage and good assembly quality. |

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

|             |                       |            |
|-------------|-----------------------|------------|
| Plate: 0182 | row: L                | column: 02 |
| Seq primer: | CACACAGGAACAGCTATGACC |            |

Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

**Location/Qualifiers**

**Source**

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/clone="UGGCM182L02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb Plasmid UGGCM library"  
/note="Vector: PMW429; Purified genomic DNA from M.  
laboratory Mouse C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of plasmid *gfi4732114(gblAF129072.1)*, a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

|                       |                 |                    |           |            |
|-----------------------|-----------------|--------------------|-----------|------------|
| Query Match           | 47.0%;          | Score 9.4;         | DB 8;     | Length 19; |
| Best Local Similarity | 90.9%;          | Pred. No. 6.3e+06; |           |            |
| Matches 10;           | Conservative 0; | Mismatches 1;      | Indels 0; | Gaps 0;    |

|    |    |             |    |
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| QY | 6  | TTGCAGGAAGC | 16 |
|    |    |             |    |
| Db | 16 | TTGCAAGAAGC | 6  |

|            |  |
|------------|--|
| RESULT     | 7  |
| AZ816318   |  |
| LOCUS      |  |
| DEFINITION | AZ816318 19 bp DNA linear GSS 20-FEB-2001                        |
|            | M0085E05F Mouse 10kb plasmid UUCGCM library Mus musculus genomic |
|            | clone UUCGCM0085E05 F, genomic survey sequence.                  |

|           |             |
|-----------|-------------|
| ACCESSION | AZ816318    |
| VERSION   | AZ816318.1  |
|           | GI:12986226 |

**SOURCE** *Mus musculus* (house mouse)

ORGANISM

## REFERENCE AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
COMMENT

**JOURNAL COMMENT**  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.000

Plate: 0085 row: E column: 05  
Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

Location/Qualifiers

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1. .19  
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/mol\_type="genomic DNA"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCGM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 47.0%; Score 9.4; DB 8; Length 19;  
Best Local Similarity 90.9%; Pred. No. 6.3e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AGGAGCGCT 20  
|||||  
2 AGGAGCGCT 12

Db

RESULT 8  
A2798282/c 20 bp DNA linear GSS 16-FEB-2001  
LOCUS 2M0055H05F Mouse 10kb plasmid UUCGM library Mus musculus genomic  
DEFINITION clone UUCGM0055H05 F, genomic survey sequence.  
ACCESSION A2798282  
VERSION A2798282.1 GI:12948227  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0055 row: H column: 05  
Seq primer: CGTTGTAAACGACGCGCAGC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

source  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGM0055H05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCGM library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 47.0%; Score 9.4; DB 8; Length 20;  
Best Local Similarity 90.9%; Pred. No. 6.4e+06;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGACG 12  
|||||  
16 ACTCTTGACG 6

Db

RESULT 9  
A2482658 19 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0107L16R Mouse 10kb plasmid UUCGM library Mus musculus genomic  
DEFINITION clone UUCGM0307L16 R, genomic survey sequence.  
ACCESSION A2482658  
VERSION A2482658.1 GI:10645919  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0307 row: L column: 16  
Seq primer: CACACAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

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1..19
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0307L16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42m; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

ORIGIN

Query Match  
Best Local Similarity 45.0%; Score 9; DB 8; Length 19;  
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTCTGCAGGAACGGC 19  
|||||  
3 CTCTGCAGGTTACTGC 19

Db

RESULT 10  
LOCUS CL661094 19 bp DNA linear GSS 09-JUL-2004  
DEFINITION PRI0138d\_F10 - PRI0138d.B21 (19) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
ACCESSION CL661094 GI:50147102  
VERSION CL661094.1 GI:50147102  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 19)  
Srinivasan,J., Octo,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an Acedb database for the nematode satellite organism Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
Contract: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.  
Location/Qualifiers  
1..19  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"

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/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/notes="Vector: pBpifos-5 Fosmid vector"
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ORIGIN

Query Match  
Best Local Similarity 45.0%; Score 9; DB 9; Length 19;  
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TCTTCAGGAACGGCT 20  
|||||  
1 TCTCGTACCAAAAGCT 17

Db

RESULT 11  
LOCUS BX559186 20 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX559186 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans CDNA clone Tse42b02\_q1c, mRNA sequence.  
ACCESSION BX559186 GI:33366480  
VERSION BX559186.1 GI:33366480  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
1 (bases 1 to 20)  
Lehane,M.J., Aksoy,S., Gibson,M., Keshornou,A., Berrihan,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2NW  
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
source  
1..20  
Location/Qualifiers  
/organism="Glossina morsitans morsitans"  
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/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse42b02\_q1c"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/note="country: zimbabwe; EST from adult gut infected with T. brucei"

ORIGIN

Query Match  
Best Local Similarity 45.0%; Score 9; DB 5; Length 20;  
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTCTGCAGGAACGGC 19  
|||||  
3 CTCTAGTAAGAGTGAC 19

Db

RESULT 12

B0587767/c  
 LOCUS B0587767 16 bp mRNA linear EST 06-DEC-2002  
 DEFINITION B012340w-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA  
 clone 024-010-M01-5-PRIME, mRNA sequence.  
 ACCESSION B0587767  
 VERSION B0587767.1 GI:26117349  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H., and Radehof, U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J 32 (5), 845-857 (2002)  
 MEDLINE 12472698  
 PUBMED 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MP1Z  
 Max-planck-institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mp1z-koeln.mpg.de  
 Insert length: 16 Std Error: 0.00  
 Plate: 10 row: M column: 01  
 Seq primer: SP6: CATACGATTGCTACACTATAG.  
 Location/Qualifiers  
 1..16  
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 /db\_xref="GABI:185096"  
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 /clone="024-010-M01"  
 /tissue\_type="leaf"  
 /lab\_host="EMDHI0B"  
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 /note="Vector: PCMSPORT6, Site 1: SalI, Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinanwaldbener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCACGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7. Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 44.0%; Score 8.8; DB 5; Length 16;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+07;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TTGACGAGGCG 17  
 DB 16 TTGACGAGGAG 5

RESULT 13  
 AZ481008 19 bp DNA linear GSS 04-OCT-2000  
 LOCUS AZ481008  
 DEFINITION 1M0302N15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0302N15 R, genomic survey sequence.  
 ACCESSION AZ481008  
 VERSION AZ481008.1 GI:10641989  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0302 row: N column: 15  
 Seq primer: CACACGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence step: 19.  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
 /clone="UUGC1M0302N15"  
 /sex="Male"  
 /lab\_host="R. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI:4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 44.0%; Score 8.8; DB 8; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+07;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CAGGAAGCGCT 20  
 DB 18 CAGGAAGCGACT 7

RESULT 14  
 AZ959942 19 bp DNA linear GSS 27-APR-2001  
 LOCUS AZ959942/c  
 DEFINITION 2M0227L13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0227L13 R, genomic survey sequence.  
 ACCESSION AZ959942  
 VERSION AZ959942.1 GI:13831169  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0227 row: L column: 13  
Seq primer: CACACAGAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UTGCM2027L13"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCM2M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF139072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
Query Match 44.0%; Score 8.8; DB 8; Length 19;  
Best Local Similarity 83.3%; Pred. No. 1.2e+07;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTTCGAGGAG 15  
| | | | |  
| | | | |  
Db 13 TATTCGAGCAAG 2

RESULT 15  
AJ599745 20 bp DNA linear GSS 15-JAN-2004  
AJ599745/c  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 492609, genomic survey sequence.  
ACCESSION  
AJ599745  
VERSION  
AJ599745.1 GI:37949373  
KEYWORDS  
GSS; left border; T-DNA flanking sequence.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana

REFERENCE  
AUTHORS  
1  
Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., Dekose,R., Pelletier,G., Lepoint,C., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL  
MEDLINE  
22363535  
PUBMED  
12446565  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsegp.versailles.inra.fr/publicines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

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/organism="Arabidopsis thaliana"  
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/cultivar="Massillawekija"  
/db\_xref="taxon:3702"  
/clone="492609"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/note="T-DNA flanking sequence left border"

misc\_feature  
1..20  
left border"

ORIGIN  
Query Match 43.0%; Score 8.6; DB 9; Length 20;  
Best Local Similarity 73.3%; Pred. No. 1.6e+07;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACTCTTCGAGGAGC 16  
| | | | |  
| | | | |  
Db 17 ACTGTTCCAGAGC 3

RESULT 16  
AJ587896 16 bp DNA linear GSS 15-JAN-2004  
AJ587896  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 337H10, genomic survey sequence.  
ACCESSION  
AJ587896  
VERSION  
AJ587896.1 GI:37937520  
KEYWORDS  
GSS; left border; T-DNA flanking sequence.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS  
1  
Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., Dekose,R., Pelletier,G., Lepoint,C., Caboche,M. and Lecharny,A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL  
MEDLINE  
22363535  
PUBMED  
12446565  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsegp.versailles.inra.fr/publicines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

**AUTHORS** Balzerque, S.  
**TITLE** Direct Substitution  
**JOURNAL** Submitted (23-OCT-2003) Balzerque S., URGV, INRA/CNRS, 2 rue Gaston Creteilux, 91057 Evry cedex, FRANCE

**COMMENT** PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

**FEATURES**  
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 /cultivar="Massillaeski1a"  
 /db\_xref="taxon:3702"  
 /clone="337H10"  
 /clone\_1ib="Arabidopsis thaliana T-DNA insertion lines"  
 /note="T-DNA flanking sequence  
 left border"

**ORIGIN**

Query Match 42.0%; Score 8.4; DB 9; Length 16;  
 Best Local Similarity 90.0%; Pred. No. 1.9e+07;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 4 TCTTCGAGGA 13  
 |||||  
 3 TCTTCGAGGA 12

**RESULT 17**  
**AZ397615/c** 19 bp DNA linear GSS 03-OCT-2000  
**LOCUS** 1M0162M07R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
**DEFINITION** clone UGCG1M0162M07 R, genomic survey sequence.

**ACCESSION** AZ397615  
**VERSION** AZ397615.1 GI:10512687  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus  
**ORGANISM** Mus musculus (house mouse)

**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

**FEATURES**  
 source  
 1. 19  
 /organism="Mus musculus"

**ORIGIN**

Query Match 42.0%; Score 8.4; DB 8; Length 19;  
 Best Local Similarity 90.0%; Pred. No. 2e+07;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 6 TTGCAGGAG 15  
 |||||  
 11 TTACAGGAG 2

**RESULT 18**  
**AZ413661/c** 19 bp DNA linear GSS 03-OCT-2000  
**LOCUS** 1M0197107R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
**DEFINITION** clone UGCG1M0197107 R, genomic survey sequence.

**ACCESSION** AZ413661  
**VERSION** AZ413661.1 GI:10537590  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus  
**ORGANISM** Mus musculus (house mouse)

**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

**FEATURES**  
 source  
 1. 19  
 /organism="Mus musculus"

```
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0197107"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

## ORIGIN

```
Query Match      42.0%; Score 8.4; DB 8; Length 19;
Best Local Similarity 90.0%; Pred. No. 2e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 GACCTCTGCA 10
          |||||
Db       10 GACCTCTGCA 1
```

```
RESULT 19
LOCUS      AZ759607              19 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION 1M0552123F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
ACCESSION  AZ759607
VERSION     AZ759607.1 GI:12866570
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0552 row: I column: 23
            Seq primer: CGTTGTAACGACGCGCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
            Location/Qualifiers
            1..19
            /organism="Mus musculus"
```

```
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0552123"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

## ORIGIN

```
Query Match      42.0%; Score 8.4; DB 8; Length 19;
Best Local Similarity 90.0%; Pred. No. 2e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      7 TGACGAGATC 16
          |||||
Db       9 TGACGAGATC 18
```

```
RESULT 20
LOCUS      AZ597307              20 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION 1M0410N24R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
ACCESSION  AZ597307
VERSION     AZ597307.1 GI:11719413
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0410 row: N column: 24
            Seq primer: CACACAGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers
            1..20
            /organism="Mus musculus"
```

```
FEATURES
source      1..19
            /organism="Mus musculus"
```

```
FEATURES
source      1..20
            /organism="Mus musculus"
```

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0410N24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

## ORIGIN

```
Query Match      42.0%; Score 8.4; DB 8; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      3 CTCTTCGACG 12
        |||||
        7 CTCTTCGATG 16
```

RESULT 21  
A2827842 20 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0104FP03 Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG2M0104FP03 R, genomic survey sequence.

ACCESSION A2827842  
VERSION A2827842.1 GI:12397750  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0104 row: F column: 03  
Seq primer: CACACAGAAACACCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"

```
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0104FP03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

## ORIGIN

```
Query Match      42.0%; Score 8.4; DB 8; Length 20;
Best Local Similarity 66.7%; Pred. No. 2e+07;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      3 CTCTTCGACGAGCGGCT 20
        |||||
        3 CTGTGGCAAGAAACATCT 20
```

RESULT 22  
AG189193 20 bp DNA linear GSS 06-MAR-2004  
LOCUS Pan troglodytes DNA, clone: RP43-063J03.T7, genomic survey  
DEFINITION sequence.

ACCESSION AG189193  
VERSION AG189193.1 GI:45221369  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 20)  
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,  
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.  
BAC end sequences of library RP-43  
Unpublished  
JOURNAL 2 (bases 1 to 20)  
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,  
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.  
Direct Submission  
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
Bioscience and Biotechnology (KIRIB), Genome Research Center (GRC);  
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea  
(E-mail:redstone@mail.kribb.re.kr, url:http://pns.grc.kribb.re.kr/  
Tel:82-42-866-7181, Fax:82-42-860-4403)  
Clones are derived from the chimpanzee BAC library RP-43 This BAC  
end was generated during the R&D process and may have higher chance  
of clone tracking errors.  
PRIMERS  
Sequencing: T7  
LIBRARY  
Vector : pBAC3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.  
Location/Qualifiers

FEATURES  
source

FEATURES

```

source
1..20
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-063J03.77"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC library"

ORIGIN
Query Match          42.0%; Score 8.4; DB 9; Length 20;
Best Local Similarity 90.0%; Pred. No. 2e+07;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTGCAGGAAG 15
    |||||
Db 10 TTGCAGGAG 1

RESULT 23
B0789829          13 bp  mRNA  linear  EST 30-JUL-2002
LOCUS             hage002aH08 Heterobasidion annosum - Scots pine infection stage
DEFINITION        (HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion
                  annosum mixed EST library cDNA clone hage002aH08, mRNA sequence.
ACCESSION          B0789829
VERSION            B0789829.1 GI:22004791
KEYWORDS           EST.
SOURCE             Pinus sylvestris/Heterobasidion annosum mixed EST library
ORGANISM           Pinus sylvestris/Heterobasidion annosum mixed EST library
REFERENCE          1 (bases 1 to 13)
AUTHORS            Asiegbu,F.O., Nahalkova,J. and Dean,R.A.
TITLES             Selected expressed sequence tags of cDNA clones from the
                  interaction of the root rot fungus (Heterobasidion annosum) with
                  seedling roots of Scots pine (Pinus sylvestris)
                  Unpublished (2001)
JOURNAL            Dept. of Forest Mycology & Pathology
COMMENT            Swedish university of Agriculture, Box 7026,S-750 07, Uppsala,
                  Sweden
                  Tel: +46 18 67 15 98
                  Fax: +46 18 30 92 45
                  Email: Fred.Asiegbu@mykopac.slu.se
FEATURES           location/Qualifiers
                   1..13
                   /organism="Pinus sylvestris/Heterobasidion annosum mixed
                   EST library"
                   /mol_type="mRNA"
                   /db_xref="taxon:169015"
                   /clone="hage002aH08"
                   /dev_stage="Seedling roots of scots pine were infected for
                   6 days with H. annosum"
                   /clone_lib="Heterobasidion annosum - Scots pine infection
                   stage (HAGE) subtraction cDNA library"
                   /note="Vector: pT-Adv; Site 1: EcoRI; The subtractive
                   hybridization cDNA library was constructed from scots pine
                   roots infected for 6-days with mycelia of Heterobasidion
                   annosum (FPS)."

ORIGIN
Query Match          41.0%; Score 8.2; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 2.3e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTCTTGACGAAG 15
    |||||
Db 1 CTCTTACAGATG 13

RESULT 24
A1042533

```

```

LOCUS             A1042533          18 bp  mRNA  linear  EST 30-JUN-1998
DEFINITION        oy06e03.x1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA
                  clone IMAGE:1665052 3' similar to TR:Q15662 Q15662
                  TRANSCRIPTION-RELATED PROTEIN ;, mRNA sequence.
ACCESSION          A1042533
VERSION            A1042533.1 GI:3281727
KEYWORDS           EST.
SOURCE             Homo sapiens (human)
ORGANISM           Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE          1 (bases 1 to 18)
AUTHORS            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES             National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                  Tumor Gene Index
JOURNAL            Unpublished (1997)
COMMENT            Contact: Robert Strausberg, Ph.D.
                  Email: cgapdb-remail.nih.gov
                  This clone is available royalty-free through LIND; contact the
                  IMAGE Consortium (info@image.llnl.gov) for further information.
                  Trace considered overall poor quality
                  Seq primer: -40m13 fwd. Et from Amerham
                  High quality sequence stop: 1.
FEATURES           location/Qualifiers
                   1..18
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:1665052"
                   /tissue_type="senescent fibroblast"
                   /lab_host="DH10B (ampicillin resistant)"
                   /clone_lib="Soares senescent_fibroblasts_NBHSF"
                   /note="Vector: pT7T3D (Pharmacia) with a modified
                   polylinker V.TYPE: phagemid; Site 1: Not I; Site 2: Eco
                   RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                   primer 15,
                   TGTTACCAATCTGAAAGTGGAGCGGCCGCAATTTTCTTTTCTTTT 3',
                   double-stranded cDNA was size selected, ligated to Eco RI
                   adapters (Pharmacia), digested with Not I and cloned into
                   the Not I and Eco RI sites of a modified pT7T3 vector
                   (Pharmacia). Library went through one round of
                   normalization to a Cot = 5. Library constructed by Bento
                   Soares and M.Fatima Bernaldo."

ORIGIN
Query Match          41.0%; Score 8.2; DB 1; Length 18;
Best Local Similarity 76.9%; Pred. No. 2.4e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACTCTTGACGGA 13
    |||||
Db 6 GACTCTGGAAGA 18

RESULT 25
C00629            18 bp  mRNA  linear  EST 31-DEC-2002
LOCUS             HIMS0008172 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION        sequence.
ACCESSION          C00629
VERSION            C00629.1 GI:1432859
KEYWORDS           EST.
SOURCE             Homo sapiens (human)
ORGANISM           Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE          1 (bases 1 to 18)
AUTHORS            Okubo,K.
TITLES             BodyMap: human gene expression database
JOURNAL            Unpublished (1995)
COMMENT            Contact: Okubo,K.
                  Institute for Molecular and Cellular Biol
                  Osaka University

```

1-3, Yamada-oka, Suite, Osaka Pref. 565, Japan  
Tel: 06-877-5111(ex.3315)  
Email: kousaku@imb.osaka-u.ac.jp  
We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

#### FEATURES

source

1.18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="adult"  
/clone\_lib="Human adult (K.Okubo)"  
/note="One or more human adult tissue"

#### ORIGIN

Query Match 41.0%; Score 8.2; DB 6; Length 18;  
Best Local Similarity 76.9%; Pred. No. 2.4e+07;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCTTGAGGAGC 16  
|||||  
3 TCTTGCTGAAAC 15

#### RESULT 26

CL661466 18 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0139d\_G02 - PRI0139d.B21 (18) mixed stage fosmid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.

ACCESSION CL661466 GI:50147979  
VERSION CL661466.1  
KEYWORDS Pristionchus pacificus  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
TITLE AppaDB: an Acedb database for the nematode satellite organism  
Prisionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)

JOURNAL Contact: Sommer RJ  
COMMENT Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

#### FEATURES

source

1.18  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pBspItoS-5 Fosmid vector"

#### ORIGIN

Query Match 41.0%; Score 8.2; DB 9; Length 18;  
Best Local Similarity 76.9%; Pred. No. 2.4e+07;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACTCTTGACGA 13

|||||  
Db 2 GAATCTTCTGCA 14

RESULT 27 19 bp mRNA linear EST 28-JUN-2004  
AJ666428 CSEQRAN09 Sus scrofa cDNA clone C000003\_N10, mRNA  
LOCUS AJ666428  
DEFINITION sequence.

ACCESSION AJ666428 GI:49350879  
VERSION AJ666428.1  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.D.  
TITLE Development of cDNA and EST resources for studying reproduction and  
embryo development in pigs and cattle  
Unpublished (2004)

JOURNAL Contact: Anderson SI  
COMMENT Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred  
V0.020425.c. Vector identified by cross\_match with the -mismatch 20  
and -mismatch 12 options. Vector: BluescriptII(KS+) R. Site 1:  
ECORI R. Site 2: NotI Description: Normalised library constructed  
from pooled tissue from day 30 placentas. Clones available from UK  
Centre for Functional Genomics in Farm Animals, Roslin Institute,  
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

#### FEATURES

source

1.19  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C000003\_N10"  
/issue\_type="placenta"  
/clone\_lib="CSEQRAN09"  
/note="Vector: pBluescriptII(KS+); Site 1: EcorI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pooled tissue from day 30 placentas."

#### ORIGIN

Query Match 41.0%; Score 8.2; DB 1; Length 19;  
Best Local Similarity 76.9%; Pred. No. 2.4e+07;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GCAGGAGCGGCT 20  
|||||  
4 GCTCGAGCGCGCT 16

#### RESULT 28

B0587387 19 bp mRNA linear EST 06-DEC-2002  
LOCUS B0587387  
DEFINITION S014305-024-010-H05-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone  
024-010-H05 5-PRIME, mRNA sequence.

ACCESSION B0587387 GI:26116969  
VERSION B0587387.1  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wrick,W., Menze,A., O'Brien,D., Lehnach,H.  
and Radeklof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weisenhaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 19 Std Error: 0.00  
 Plate: 10 row: H column: 05  
 Seg primer: SP6; CATGACGATTGATGACACTATAG.  
 Location/Qualifiers

FEATURES  
 source  
 1..19  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultiivar="RWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:185481"  
 /db\_xref="taxon:161934"  
 /clone="024-010-H05"  
 /issue\_type="leaf"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MPiz-ADIS-024-leaf"  
 /note="Vector: PCWVSP0R6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatnucht AG Binbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

# ORIGIN

Query Match 41.0%; Score 8.2; DB 5; Length 19;  
 Best Local Similarity 76.9%; Pred. No. 2.4e+07;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTTCTGCAGGAAG 15  
 |||||  
 DB 6 CTCTGGCCGCAAG 18

RESULT 29  
 A2363824 19 bp DNA linear GSS 02-OCT-2000  
 LOCUS 1M0109P06R Mouse 10kb plasmid UGCIIM library Mus musculus genomic  
 DEFINITION clone UGCIIM0109P06 R, genomic survey sequence.  
 ACCESSION A2363824  
 VERSION A2363824.1 GI:10477524  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00  
 Plate: 0109 row: P column: 06  
 Seg primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
 1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCIIM0109P06"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCIIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES  
 source

# ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;  
 Best Local Similarity 76.9%; Pred. No. 2.4e+07;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTTGCAGGAGCG 17  
 |||||  
 DB 1 CTGACAGGAAGTG 13

RESULT 30  
 A2422762 19 bp DNA linear GSS 03-OCT-2000  
 LOCUS 1M0201P12R Mouse 10kb plasmid UGCIIM library Mus musculus genomic  
 DEFINITION clone UGCIIM0201P12 R, genomic survey sequence.  
 ACCESSION A2422762  
 VERSION A2422762.1 GI:10546871  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00  
Plate: 0201 row: P column: 12  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGCM0201P12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCGCM library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;  
Best Local Similarity 76.9%; Pred. No. 2.4e+07;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TTGCAGGAGCGG 18  
Db 19 TTGCAGGAGCGG 7

## RESULT 31

AZ509071

LOCUS 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION IM0351A21R Mouse 10kb plasmid UUCGCM library Mus musculus genomic  
clone UUCGCM0351A21 R, genomic survey sequence.

ACCESSION

AZ509071

VERSION

KEYWORDS

SOURCE

ORGANISM

GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE

Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

JOURNAL

COMMENT

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0351 row: A column: 21  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGCM0351A21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCGCM library"  
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;  
Best Local Similarity 76.9%; Pred. No. 2.4e+07;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TTGCAGGAGCGG 19  
Db 1 TTGCAGGAGCGG 13

## RESULT 32

AZ626779

LOCUS 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0467A14F Mouse 10kb plasmid UUCGCM library Mus musculus genomic  
clone UUCGCM0467A14 F, genomic survey sequence.

ACCESSION

AZ626779

VERSION

KEYWORDS

SOURCE

ORGANISM

GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE

Unpublished (2000)  
Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

JOURNAL

COMMENT

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0467 row: A column: 14  
 Seq primer: CCTGTGTAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

# FEATURES

source

Location/Qualifiers

1..19

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0467A14"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

## Query Match

Best Local Similarity 41.0%; Score 8.2; DB 8; Length 19;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTCCTTGACGAG 15  
 |||||  
 DB 4 CACTTTCAGGAG 16

## RESULT 33

AZ410583

LOCUS

1M0182E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0182E24 R, genomic survey sequence.

ACCESSION

AZ410583.1 GI:10534512

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0182 row: E column: 24  
 Seq primer: CACACGAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

# FEATURES

source

Location/Qualifiers

1..20

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0182E24"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1ib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

## Query Match

Best Local Similarity 41.0%; Score 8.2; DB 8; Length 20;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACTCTTGACGAG 13  
 |||||  
 DB 4 GATCTTCCAGCA 16

## RESULT 34

TA207B030/c

LOCUS

T. brucei sheared genomic DNA clone 207B03, reverse sequence, genomic survey sequence.

ACCESSION

AL475823.1 GI:11842591

VERSION

KEYWORDS

SOURCE

ORGANISM

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE

AUTHORS

1 (bases 1 to 20)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaundin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

## source

1.20  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="207b03"

## ORIGIN

Query Match 41.0%; Score 8.2; DB 9; Length 20;  
Best Local Similarity 76.9%; Pred. No. 2.5e+07;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCGAGA 13  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 GCTCATGCGAGA 7

RESULT 35  
AA916934 19 bp mRNA linear EST 17-JUN-1998  
LOCUS on14a09.g1 NCI CGAP LUS Homo sapiens CDNA clone IMAGE:1556632 3'  
DEFINITION similar to SW:BI3\_MOUSE P28662 BRAIN PROTEIN I3 ; mRNA sequence.  
ACCESSION AA916934  
VERSION AA916934.1 GI:3056326  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 19)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNM at: [www-bio.11nl.gov/bdrip/image/image.html](http://www-bio.11nl.gov/bdrip/image/image.html)

## JOURNAL COMMENT

Trace considered overall poor quality  
Insert Length: 444 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

## source

1.19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1556632"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP LUS"  
/note="Organ: lung; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from a neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaudo. "

## ORIGIN

Query Match 40.0%; Score 8; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTGCAGGA 13  
| | | | | | | | | | | | | | | | | | | | | |  
Db 8 TTGCAGGA 1

RESULT 36  
CNS09MAX 19 bp mRNA linear HTC 08-JAN-2003  
LOCUS Single read from an extremity of a full-length cDNA made from  
DEFINITION Anopheles gambiae total adult females 3-PRIME end of clone  
FR0AAC48CF12 of strain 6-9 of Anopheles gambiae (African malaria mosquito).  
BX064981  
ACCESSION BX064981.1 GI:27638262  
VERSION  
KEYWORDS  
SOURCE HTC.  
ORGANISM Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
1 (bases 1 to 19)  
Genoscope.  
Direct Submission  
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr) - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
Location/Qualifiers

## FEATURES

## source

1.19  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="6-9"  
/db\_xref="taxon:7165"  
/clone="FR0AAC48CF12"  
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/note="end : 3-PRIME"

## ORIGIN

Query Match 40.0%; Score 8; DB 3; Length 19;  
Best Local Similarity 68.8%; Pred. No. 3.1e+07;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CTCTTCAGGAGACGG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 CCGGCGACGAGAGGG 4

RESULT 37  
AZ500630 19 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0339A10F Mouse 10kb plasmid UUGCM library Mus musculus genomic  
DEFINITION clone UUGCM0339A10 F, genomic survey sequence.  
ACCESSION AZ500630  
VERSION AZ500630.1 GI:10680639  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D. Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL COMMENT

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0339 row: A column: 10  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddum@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0082 row: P column: 13  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

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/organism="Mus musculus"  
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 40.0%; Score 8; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CAGGAGC 16  
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Db 3 CAGGAGC 10

RESULT 38  
AZ814554/c 19 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0082P13.F Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCGCM0082P13 F, genomic survey sequence.  
ACCESSION AZ814554  
VERSION AZ814554.1 GI:12984462  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D. Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center

1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 40.0%; Score 8; DB 8; Length 19;  
Best Local Similarity 68.8%; Pred. No. 3.1e+07;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 TCTTCAGGAGCGGC 19  
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Db 16 TCACACAGGAAACAGC 1

RESULT 39  
CF305590 20 bp mRNA EST 15-AUG-2003  
LOCUS HDAL-01-C09.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA  
clone HDAL-01-C09, mRNA sequence.  
ACCESSION CF305590  
VERSION CF305590.1 GI:33677351  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 20)  
Kim, J.S., Jun, K.M., Cheong, P.D., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
JOURNAL Contact: Nahm B.H.  
COMMENT of Bioscience and Bioinformatics, Myongji University

Yongjin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers

1. .20  
 /organism="Oryza sativa (japonica cultivar-group)"  
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 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## ORIGIN

Query Match 40.0%; Score 8; DB 7; Length 20;  
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 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TGCAGGA 14  
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 Db 4 TGCAGGA 11

RESULT 40 20 bp DNA linear GSS 02-OCT-2000  
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 DEFINITION clone UNGCM0115N07 R, genomic survey sequence.

ACCESSION AZ366451 GI:10480151  
 VERSION AZ366451  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D. Weiser,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 015 row: N column: 07  
 Seq primer: CACACAGGAACAGCTATGAC  
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 Location/Qualifiers

## FEATURES

1. .20  
 /organism="Mus musculus"  
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 /clone="UNGCM0115N07"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UNGCM library"  
 /note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 40.0%; Score 8; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+07;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AGGAGCG 17  
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 Db 6 AGGAGCG 13

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 Job time : 1629 secs

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